

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 20:24:38 ; Search time 88 Seconds
(without alignments)
1372.371 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKWNILIPVHIGNANK 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_todent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2248	91.5	475	Q8SPU7	Q8spu7 bos taurus
2	2085.5	84.9	432	11 Q9QXK6	Q9qxx6 mus musculus
3	1623.5	56.1	363	11 Q8BIE9	Q8bie9 mus musculus
4	1572.5	64.0	462	13 Q8AV68	Q8av68 brachydanio
5	1526	62.1	464	11 Q8R5H3	Q8r5h3 mus musculus
6	1526	62.1	464	11 Q8BWN3	Q8bwn3 mus musculus
7	1427.5	58.1	449	11 Q9CYK8	Q9cyk8 mus musculus
8	1186.5	48.3	512	11 Q91X60	Q91x60 mus musculus
9	1153.5	47.0	629	11 Q9ET51	Q9et51 mus musculus
10	1147	46.7	494	11 Q8KOA7	Q8koa7 mus musculus
11	1144.5	46.6	629	11 Q8BHE9	Q8bhe9 mus musculus
12	1139	46.4	494	11 Q9ROW9	Q9row9 mus musculus
13	1097.5	44.7	499	11 Q8VHH6	Q8vhh6 mus musculus
14	1097.5	44.7	499	11 Q8R4G9	Q8r4g9 mus musculus
15	1097.5	44.7	504	11 Q8BV44	Q8bv44 mus musculus
16	1075.5	43.8	536	5 Q8TOY9	Q8toy9 aplysia cal

17	1074.5	43.8	536	5	Q8T9S0	Q8t9s0 aplysia cal
18	1065.5	43.4	515	5	Q46133	Q46133 locusta mig
19	1064.5	43.3	537	5	Q8MUR0	Q8mur0 apis mellif
20	1062.5	43.3	523	5	Q46128	Q46128 heliothis v
21	1051	42.8	531	5	Q96632	Q96632 heliothis v
22	1045.5	42.6	502	5	Q9N587	Q9n587 caenorhabdi
23	1039	42.3	533	5	Q8WRS1	Q8wrs1 chilo suppr
24	1025.5	41.8	567	5	Q9VC74	Q9vc74 drosophila
25	1024.5	41.7	537	5	Q9U941	Q9u941 myzus persi
26	1015	41.3	495	11	Q8R493	Q8r493 mus musculu
27	1009.5	41.1	489	4	Q9RR84	Q9rrr4 homo sapien
28	1004	40.9	457	6	Q9XS62	Q9xs62 canis famli
29	1002.5	40.8	532	5	Q9U940	Q9u940 myzus persi
30	1002	40.8	496	6	Q8SPU6	Q8spu6 bos taurus
31	995.5	40.5	532	5	Q8MUR6	Q8mur6 aphid gossy
32	989	40.3	545	5	Q96631	Q96631 heliothis v
33	980	39.9	501	11	Q9ERK7	Q9erk7 mus musculu
34	980	39.9	501	11	Q9R291	Q9r291 mus musculu
35	980	39.9	501	11	Q8BGP7	Q8bgp7 mus musculu
36	979.5	39.9	568	5	Q9NFR5	Q9nfr5 drosophila
37	970.5	39.5	540	5	Q46134	Q46134 locusta mig
38	964.5	39.3	341	11	Q8V111	Q8v111 mus musculu
39	962.5	39.2	595	5	P91764	P91764 myzus persi
40	962	39.2	500	11	Q9ROC3	Q9roc3 mus musculu
41	935.5	38.1	559	5	Q46132	Q46132 locusta mig
42	929	37.8	552	5	P91765	P91765 myzus persi
43	918.5	37.4	497	5	Q46135	Q46135 locusta mig
44	918.5	37.4	509	5	Q9NFX8	Q9nfx8 myzus persi
45	915.5	37.3	795	5	Q18394	Q18394 drosophila

ALIGNMENTS

RESULT 1

ID	Q8SPU7	PRELIMINARY;	PRT;	475 AA.
AC	Q8SPU7;			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Neuronal nicotinic acetylcholine receptor alpha5 subunit.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97156643; PubMed=9003033;			
RA	Campos-Caro A., Smillie F.I., Dominguez del Toro E., Rovira J.C.,			
RA	Vicente-Agullo F., Chapuli J., Juiz J.M., Sala S., Sala F.,			
RA	Ballesta J.J., Criado M.;			
RT	"Neuronal nicotinic acetylcholine receptors on bovine chromaffin			
RT	cells: cloning, expression, and genomic organization of receptor			
RT	subunits.";			
RT	J. Neurochem. 68:488-497(1997).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RA	Campos-Caro A., Criado M.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.			
DR	EMBL; AF187464; AAL88711.1; -			
DR	InterPro; IPR006201; Neur_chan.			
DR	InterPro; IPR006202; Neur_chan_LBD.			
DR	InterPro; IPR006029; Neu_chan_memb.			
DR	Pfam; PF02931; Neur_chan_LBD; 1			
DR	Pfam; PF02932; Neur_chan_memb; 1			
DR	TIGRFAMs; TIGR00860; LIC; 1.			
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.			
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;			
KW	Transmembrane.			

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SQ SEQUENCE 475 AA; 54259 MW; 24658023DF0E3D1A CRC64;
Query Match 91.5%; Score 2248; DB 6; Length 475;
Best Local Similarity 90.3%; Pred. No. 5,7e-180;
Matches 419; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 5 GSGPRAURLLLLVNAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYERWVRP 64
DB 12 GLGFLQLQVLPFLVAGRWGPEGAGGVRGLAEPVWAKHEDSLFQDLFQDYERWVRP 71
QY 65 VEHLNDKIKFKGLAISQLVDVDEKQMLMTNWLKQEWIDVLRWNPDDYGGIKVIRP 124
DB 72 VEHLNDKIKFKGLAISQLVDVDEKQMLMTNWLKQEWIDVLRWNPDDYGGIKVIRP 131
QY 125 SDSVWTPDILVFNADGRFGSTKTVIRYNGVTWTPPPANYKSSCTIDVTFPPFDLQNC 184
DB 132 SDSLWTFDILVFNADGRFGSTKTVIRYNGVTWTPPPANYKSSCTIDVTFPPFDLQNC 191
QY 185 SMKFGSWTYDGSQVDIILEDDQVDKDRDFDNGEWEIVSATGSKGNRTDSCWYPYTYSF 244
DB 192 SMKFGSWTYDGSQVDIILEDDQVDKDRDFDNGEWEIVSATGSKGNRTDSCWYPYTYSF 251
QY 245 VIKRLPLFYTLFLIIPICIGLSFLTVLYPLSPNEGEKICLCTSVLSLTVFLVLIBEIIIP 304
DB 252 VIKRLPLFYTLFLIIPICIGLSFLTVLYPLSPNEGEKICLCTSVLSLTVFLVLIBEIIIP 311
QY 305 SSSKVIPLICEYLVTMIFVTLTSMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTLPKLL 364
DB 312 SSSKVIPLICEYLVTMIFVTLTSMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTLPKLL 371
QY 365 CMRSHVDYRFTQKEETSGSGPKSSRNTLEAALNSIRYITRHKENDVREVEDWKFIA 424
DB 372 CMRSHVDYRFTQKEETSGSGPKSSRNTLEAALNSIRYITRHKENDVREVEDWKFIA 431
QY 425 QVLDRLMFLWTFVSVISVGLFVPVIYKXANLIPVHIGNANK 468
DB 432 QVLDRLMFLWTFVSVISVGLFVPVIYKXANLIPVHIGNANK 475

RESULT 2
Q9QXK6 PRELIMINARY; PRT; 432 AA.
AC Q9QXK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 5 subunit (Fragment).
GN ACR45.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/21bg; TISSUE=Interpeduncular nucleus of brain;
RA Stitzel J.A., Blanchette J.M.;
RT "Cloning of mouse nicotinic receptor alpha 5 subunit cDNA.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF204689; AFI9423.1; -.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
FT NON_TER
SQ SEQUENCE 432 AA; 49635 MW; 640881B448C4FD4C CRC64;

Query Match 84.9%; Score 2085.5; DB 11; Length 432;
Best Local Similarity 90.1%; Pred. No. 2,1e-166;
Matches 390; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 36 GLSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKQMLMTT 95
DB 1 GVEPLSSAAKHEDSLFQDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKQMLMTT 60
QY 96 NWLWKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDILVFNADGRFGSTKTVIRYN 155
DB 61 NWLWKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDILVFNADGRFGSTKTVIRYN 120
QY 156 GTVWTPPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDDQVDKDRFFDN 215
DB 121 GTVWTPPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDDQVDKDRFFDN 180
QY 216 GWMEIVSATGSKGNRTDSCWYPYTYSFVVKRLPLFYTLFLIIPICIGLSFLTVLYPL 275
DB 181 GEWEIMSMGSKGNRTDSCWYPYTYSFVVKRLPLFYTLFLIIPICIGLSFLTVLYPL 240
QY 276 SNEGEKICLCTSVLSLTVFLVLIBEIIIPSSSKVIPLICEYLVTMIFVTLTSMVTVFAI 335
DB 241 SNEGEKICLCTSVLSLTVFLVLIBEIIIPSSSKVIPLICEYLVTMIFVTLTSMVTVFAI 300
QY 336 NIHRSSSTHNAMAPLVKIFLHTLPKLLCMRSHVDYRFTQKEETSGSGPKSSRNTLEA 395
DB 301 NIHRSSSTHNAMAPLVKIFLHTLPKLLCMRSHVDYRFTQKEETSGSGPKSSRNTLEA 359
QY 396 ALNSIRYITRHKENDVREVEDWKFIAQVLDRLMFLWTFVSVISVGLFVPVIYKXANL 455
DB 360 ALDCIRYITRHKENDVREVEDWKFIAQVLDRLMFLWTFVSVISVGLFVPVIYKXANL 419
QY 456 NTLIPVHIGNANK 468
DB 420 NTLIPVHIGNANK 432

RESULT 3
Q8BIE9 PRELIMINARY; PRT; 363 AA.
AC Q8BIE9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NICOTINIC receptor alpha 5 subunit homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/60; TISSUE=Adipose tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080900; BAC38070.1; -.
SQ SEQUENCE 363 AA; 41327 MW; BFC17A2AE1146DC1 CRC64;

Query Match 66.1%; Score 1623.5; DB 11; Length 363;
Best Local Similarity 68.8%; Pred. No. 9e-128;
Matches 322; Conservative 17; Mismatches 24; Indels 105; Gaps 2;

QY 1 MAARGSGPRALLLLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 60
DB 1 MAARGSGPRALLLLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 34
QY 61 WVRPVEHLNDKIKFKGLAISQLVDVDEKQMLMTNWLKQEWIDVLRWNPDDYGGIKV 120
DB 35 ----- 34
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QY 121 IRVPSVSWTPDVLVDNADGRFEGSTKTIVRYNGTIVTTPPANYKSSCTIDVTFPPD 180
 DB 35 -----GDGRFEGASTKTIVRYNGTIVTTPPANYKSSCTIDVTFPPD 76
 QY 181 LONCSMKFGSWTYDGSQVDIILEDDVDKDRDFDNGEWEIFSATGSKGNRTDSCCWYPV 240
 DB 77 LONCSMKFGSWTYDGSQVDIILEDDVDKDRDFDNGEWEIFSATGSKGNRTDSCCWYP 136
 QY 241 TYSFVTKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGEKICLCTSVLSVLTFLVIE 300
 DB 137 TYSFVTKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGEKICLCTSVLSVLTFLVIE 196
 QY 301 EIIPSSKVIPLIGEVLVFTMTVLTSLIMVTFAINIHRRSSSTHNAAPLVKRIPLHTL 360
 DB 197 EIIPSSKVIPLIGEVLVFTMTVLTSLIMVTFAINIHRRSSSTHNAAPLVKRIPLHTL 256
 QY 361 PKLLCNRSHVDRYFQKEETESGSKSRNTLEALNSIRYTRHMKENDVREVEDW 420
 DB 257 PKLLCNRSHVDRYFQKEETESGSKSRNTLEALNSIRYTRHMKENDVREVEDW 315
 QY 421 KFAQVLDKRLMTLFLFVSIIVGSLGFLFVPIVYKWNILIPVHIGNANK 468
 DB 316 KFAQVLDKRLMTLFLFVSIIVGSLGFLFVPIVYKWNILIPVHIGNANK 363

RESULT 4

Q8AV68 PRELIMINARY; PRT; 462 AA.
 ID Q8AV68
 AC Q8AV68
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nicotinic acetylcholine receptor beta3 subunit.
 GN NACHR-BETA3.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22338858; PubMed=12451132;
 RA Tokuda H., Yoshida T., Matsuda N., Mishina M.;
 RT "Regulation by Glycogen Synthase Kinase-3beta of the Arborization
 Field and Maturation of Retinorectal Projection in Zebrafish."
 RL J. Neurosci. 22:10324-10332(2002).
 DR EMBL; AB087185; BAC41198.1; -.
 KW Receptor.
 SQ SEQUENCE 462 AA; 53197 MW; 9F396990DBA30964 CRC64;

Query Match 64.0%; Score 1572.5; DB 13; Length 462;
 Best Local Similarity 67.8%; Pred. No. 2.3e-123;
 Matches 288; Conservative 63; Mismatches 59; Indels 15; Gaps 3;
 QY 42 STAKHEDSLKDLFDYERWRVPVHNDKIKIKFGLAISQVLDVDEKKNQMTTNVWLKQ 101
 DB 26 SLAEREDALLRLDFQYQWRVPILHANTVKVRFGLKISQVLDVDEKKNQMTTNVWLYE 85
 QY 102 EMDVLRNPDYGGIKVIRVPSVSWTPDVLVDNADGRFEGT-STKTIVRYNGTIVT 160
 DB 86 EMDVLRNPDYGGIKVIRVPSVSWTPDVLVDNADGRFEGT-STKTIVRYNGTIVT 145
 QY 161 TTPANYKSSCTIDVTFPPDLONCSMKFGSWTYDGSQVDIILEDDVDKDRDFDNGEWEIF 220
 DB 146 TTPANYKSSCTIDVTFPPDLONCSMKFGSWTYDGSQVDIILEDDVDKDRDFDNGEWEIF 205
 QY 221 VSATGSKGNRTDSCCWYPVYTSFVTKRLPLFTLLIIPICIGLSPLTVLVFVLPNSGE 280
 DB 206 VSATGSKGNRTDSCCWYPVYTSFVTKRLPLFTLLIIPICIGLSPLTVLVFVLPNSGE 265
 QY 281 KICLCTSVLSVLTFLVLTVEEIPSSSKVIPLIGEVLVFTMTVLTSLIMVTFAINIHHR 340

DB 266 KVSLSVLSVLTFLVLTVEEIPSSSKVIPLIGEVLVFTMTVLTSLIMVTFAINIHHR 325
 QY 341 SSSTHNAAPLVKRIPLHTLPLKLLCNRSHVDRYFQKEETESGSKPKSSR----- 390
 DB 326 SSATVHPSPWVRLTFLQRLPDLCCMRGNTDRYHPQMPQSPDLKPKSKGPPGPGD 385
 QY 391 -----NTLEAALNSIRYTRHMKENDVREVEDWKFIAQVLDKRLMTLFLFVSIIVGSLG 446
 DB 386 QALINMLEQATNSVRYISRHKKHFIREVQDMKFVAQVLDRIFLWAFLTVSVLGTILI 445
 QY 447 FVPIV 451
 DB 446 FTPAV 450

RESULT 5

Q8RSH3 PRELIMINARY; PRT; 464 AA.
 ID Q8RSH3
 AC Q8RSH3
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nicotinic acetylcholine receptor beta 3 subunit.
 GN CHRN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stitzel J.A., Lautner M.A., Jimenez M., Bhandarkar S.J., Curtis C.D.,
 RA Remias J.;
 RT "Isolation of a mouse nicotinic acetylcholine receptor Beta 3 subunit
 cDNA."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 DR EMBL; AF467896; AAL75573.1; -.
 DR InterPro; IPR006201; Neur channel.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006029; Neur_chan_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
 KW Transmembrane.
 SQ SEQUENCE 464 AA; 53140 MW; 823AB7B250D72034 CRC64;

Query Match 62.1%; Score 1526; DB 11; Length 464;
 Best Local Similarity 65.8%; Pred. No. 1.8e-119;
 Matches 289; Conservative 66; Mismatches 64; Indels 20; Gaps 4;
 QY 33 AQRGLSEPSIAKHEDSLKDLFDYERWRVPVHNDKIKIKFGLAISQVLDVDEKKNQ 92
 DB 24 ATAGL-----SSVAEHEDALLRLDFQYQWRVPVLSNDIIKVFGLKISQVLDVDEKKNQ 80
 QY 93 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSVSWTPDVLVDNADGRFEGT-STKTIV 151
 DB 81 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSVSWTPDVLVDNADGRFEGT-STKTIV 140
 QY 152 IRYNGTIVTTPPANYKSSCTIDVTFPPDLONCSMKFGSWTYDGSQVDIILEDDVDKDR 211
 DB 141 VKSSGTSVSWTPASYKSSCTMDVTFPPDLONCSMKFGSWTYDGSQVDIILEDDVDKDR 200
 QY 212 FFDNGEWEIFSATGSKGNRTDSCCWYPVYTSFVTKRLPLFTLLIIPICIGLSPLTVLV 271
 DB 201 FFDNGEWEIFSATGSKGNRTDSCCWYPVYTSFVTKRLPLFTLLIIPICIGLSPLTVLV 260
 QY 272 FYLPSNDEGEKICLCTSVLSVLTFLVLTVEEIPSSSKVIPLIGEVLVFTMTVLTSLIMVT 331
 DB 261 FYLPSNDEGEKICLCTSVLSVLTFLVLTVEEIPSSSKVIPLIGEVLVFTMTVLTSLIMVT 320

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QY 332 VFAINIHRRSSSTHNAMAPLVKIFLHTLPKLLCMRSHVDYF-----TOKEETESGGPK 387
DB 321 VFVINVHRSSSTVHPNAPVWKRLFLEKLPWLCKDPRDRFSPDGTESKGTGVRGKFGP 380
QY 388 SSRNT-----LEALNSIRYITRHKENDVREVVEDKFIQVLDRLMELWTF 435
DB 381 KKQOTPTSDGERVLVAFLEKASESIRYISRVKKEHFIQVQVDKFWAQLDRIFLWLF 440
QY 436 LFVSIIVGSLGLFVPVIYKW 454
DB 441 LTASVLGSLVIFIPALQKW 459

RESULT 6
Q8BMN3 PRELIMINARY; PRT; 464 AA.
AC Q8BMN3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuronal acetylcholine receptor protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK030464; BAC26973.1; -.
SQ SEQUENCE 464 AA; 53112 MW; 2CEA3E0DAF2D5EB CRC64;

Query Match 62.1%; Score 1526; DB 11; Length 464;
Best Local Similarity 65.8%; Pred. No. 1.8e-119;
Matches 289; Conservative 66; Mismatches 64; Indels 20; Gaps 4;
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```
QY 33 AQRLSPSSIAKHEDSLKDLFDYERWVRVPEHLNDKIKIFGLAISQLVDVDEKNQL 92
DB 24 ATAGL---SSVAEHEDALLRHFLFGYQKCVRPVNLSSDIIKVFGLKISQLVDVDEKNQL 80
QY 93 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 151
DB 81 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 140
QY 152 IRYNGTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDDVDKRD 211
DB 141 VKSGTGVSWTPPASYKSSCTMDVTFPPDLQNCMKFGSWTYDGTWVDLILINENVDKRD 200
QY 212 FPDNGEWEIVSATGSKGNRTDSCCWYPTVYTSFVIRKLPFLFTLFIIPICIGLSFLTIV 271
DB 201 FPDNGEWEILNAKGMKNRREGFYSPVTVYSFVLRRLPFLFTLFIIPICIGLSFLTIV 260
QY 272 FYLPNDEGEKICLCTSVLSVLTVPFLVIBELIIPSSKVIPIGLBYLFTVFTLSIMVT 331
DB 261 FYLPNDEGEKLSLSTSVLSVLTVPFLVIBELIIPSSKVIPIGLBYLFTVFTLSIIVT 320
QY 332 VFAINIHRRSSSTHNAMAPLVKIFLHTLPKLLCMRSHVDYF-----TOKEETESGGPK 387
DB 321 VFVINVHRSSSTVHPNAPVWKRLFLEKLPWLCKDPRDRFSPDGTESKGTGVRGKFGP 380
QY 388 SSRNT-----LEALNSIRYITRHKENDVREVVEDKFIQVLDRLMELWTF 435
DB 381 KKQOTPTSDGERVLVAFLEKASESIRYISRVKKEHFIQVQVDKFWAQLDRIFLWLF 440
QY 436 LFVSIIVGSLGLFVPVIYKW 454
DB 441 LTASVLGSLVIFIPALQKW 459
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RESULT 7
Q9CYK8 PRELIMINARY; PRT; 449 AA.
AC Q9CYK8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 5730417K16RIK protein.
GN CHRN3 OR 5730417K16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AK017571; BAB30812.1; -.
DR MGD; MGI:106212; Chnrb3.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_chan_memb.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAms; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 449 AA; 51281 MW; FFS4824C5DAA8E7 CRC64;
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Query Match 58.1%; Score 1427.5; DB 11; Length 449;
Best Local Similarity 62.4%; Pred. No. 3.2e-111;
Matches 274; Conservative 66; Mismatches 64; Indels 35; Gaps 5;

QY 33 AQRLSPSSIAKHEDSLKDLFDYERWVRVPEHLNDKIKIFGLAISQLVDVDEKNQL 92
DB 24 ATAGL---SSVAEHEDALLRHFLFGYQKCVRPVNLSSDIIKVFGLKISQLVDV----- 74
QY 93 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 151
DB 75 -----EWTQKLRWNPEDYGGILNSIKVPSLSLWLPDIVLFDNADGRFEGSLMTKAI 125
QY 152 IRYNGTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDDVDKRD 211
DB 126 VKSGTGVSWTPPASYKSSCTMDVTFPPDLQNCMKFGSWTYDGTWVDLILINENVDKRD 185
QY 212 FPDNGEWEIVSATGSKGNRTDSCCWYPTVYTSFVIRKLPFLFTLFIIPICIGLSFLTIV 271
DB 186 FPDNGEWEILNAKGMKNRREGFYSPVTVYSFVLRRLPFLFTLFIIPICIGLSFLTIV 245
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QY 272 FYLPSEGEKICLCTSVLSVLTFTVLVIEIIPSSSKVPIPLGEYLVFTMIFTLSIMVT 331
Db 246 FYLPSEGEKLSLTSVLSVLTFTVLVIEIIPSSSKVPIPLGEYLVFTMIFTLSIMVT 305
QY 332 VFAINIHRSSTHNAAPLVKIFLHTLPKLLCMRSHVDRYF----TQKETESGSGPK 387
Db 306 VFVINHRSSTYHPMAPWVKLEKLPWLCKMDPRDRFSFPDGTESKGTGKPKFG 365
QY 388 SSRNT-----LEAALNSIRYTRHMKENDVREVVEDWKFIAQVLDRLMFLWTF 435
Db 366 KKKQPTSDGERVLVAFLEKASESIRYSRHVKEHFSQVQDQWKFVQVLDRLFLWLF 425
QY 436 LFVSVIGSLGLFPVPIYKW 454
Db 426 LTASVLGSLVLPFIPALKMW 444

RESULT 8
Q91X60 PRELIMINARY; PRT; 512 AA.
ID Q91X60
AC Q91X60
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Similar to cholinergic receptor, nicotinic, alpha polypeptide 2
DN (Neuronal).
GN CHRNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; BC011490; AAH1490.1; -.
DR MGD; MGI:87886; Chrna2.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 512 AA; 58735 MW; AC0C6CC398B69C6C CRC64;

Query Match 48.3%; Score 1186.5; DB 11; Length 512;
Best Local Similarity 49.3%; Pred. No. 66-91;
Matches 237; Conservative 73; Mismatches 102; Indels 69; Gaps 7;

QY 37 LSEPIIAKHEDSLKOLFQDYERWVRVPEHLNDKIKFKGLAISQVLDVDEKQNMVTN 96
Db 26 LAQQSHTHAEDRLFKHFGGYNRWAPVPTSDVIVRFGLSIAQLIDVDEKQNMVTN 85
QY 97 VWLKQEWIDVLRNPPDYGKIKIRVPSDSVWTPDIVLFONADGRFGT-STKTIVRYN 155
Db 86 VWLKQEWNDYKLRWDPAEFGNITSLRVPSEMIWIPIVLNNADGEFAVTHMTKAHLFFT 145
QY 156 GTVTWTPPANYKSSCTIDVTFPPDPLQNCMKFGSWTYDGSQVDIILEDQDVKDFFDN 215
Db 146 GTVHWVPPIAYKSSCIDVTFPPDQCKMKFGSWTYDKAKIDLEQMERTVDLKYWES 205
QY 216 GEWEIVSATGSKGNRTDSCC--WYPVYTSYFVKRLPLFTLPIICIGLSFLVLVYF 273
Db 206 GEWALINATGYNKSKYDCCAEIYPDVITYFVIRKPLPYINLIIPCLLSCLVLVYF 265
QY 274 LPSNEGEKICLCTSVLSVLTFTVLVIEIIPSSSKVPIPLGEYLVFTMIFTLSIMVT 333

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Db 266 LPSEGEKITICISVLLSLTFLVLLITEIIPSTSLVPLIGEYLLFTMIFTLSIVITVF 325
QY 334 AINIHRSSTHNAAPLVKIFLHTLPKLLCMRSHV----- 370
Db 326 VLVNHRSPSTN-MPNWVRVALLGRVPRWLMNRPPLPMBELHSGPGLKLSPTYHWELE 384
QY 371 ---DRYPTQKETES-----GS-----GPKSSRNT----- 392
Db 385 MDASEREETESEEEEDENICMCAGLPDSSMGVLYGHSLHLRANGPEAKTPSQASEIL 444
QY 393 ----LEAALNSIRYTRHMKENDVREVVEDWKFIAQVLDRLMFLWTFVSVIGSLGLFPV 448
Db 445 LSPQIQKALEGVHYIADHLRSEDASSVKEDWKYVAMVVDRIFLFIIVCFGLTGIFL 504
QY 449 P 449
Db 505 P 505

RESULT 9
Q9ET51 PRELIMINARY; PRT; 629 AA.
ID Q9ET51
AC Q9ET51
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 4 subunit.
GN CHRNA4 OR ACRA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Sleep Selected Line;
RA Stitzel J.A., Jimenez M., Smolen A., Modir J.;
RT "Cloning of mouse nicotinic acetylcholine receptor subunit alpha 4 cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF225912; AAF34716.2; -.
DR MGD; MGI:87888; Chrna4.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 629 AA; 70319 MW; 78C28BDEFE371FB2F CRC64;

Query Match 47.0%; Score 1153.5; DB 11; Length 629;
Best Local Similarity 39.8%; Pred. No. 4.6e-88;
Matches 251; Conservative 78; Mismatches 111; Indels 191; Gaps 10;

QY 1 MAARGSPRALRLRLLLVQLVAGRCGLAGAGAGQRLSEPSIIAKHEDSLKDLFDQYER 60
Db 88 MEIGSGAPPELLELLLLLLG-TGLLPAS-----SHIETRAHEERLKRFLSGYNK 52
QY 61 WRPVPEHLNDKIKFKGLAISQVLDVDEKQNMVTNVLKQEWIDVLRNPPDYGKIKV 120
Db 53 WSREPVANISDVLRVFGLSIAQLIDVDEKQNMVTNVMVKQEWHDYKLRWDGDEYNTS 112
QY 121 IRVPSDSVWTPDIVLFONADGRFGTS-TKTIVRYNGTVTTPPANYKSSCTIDVTFPPF 179
Db 113 IRIPELWIRPDIVLVNNADGNFAVTHLTKAHLFDGVRQVTPPPIAYKSSCIDVTFPPF 172
QY 180 DLQNCMKFGSWTYDGSQVDIILEDQDVKDFFDNGEWEIVSATGSKGNRTDSCC--WY 237

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Db 173 DOQNTKMGSTYDAXKIDLVMSRVDQDFWSEGEVIVDAGTVNTRKYCEAEIY 232
QY 238 PVTYSFVFKRPLFLYTLFLIIPICIGLSFLTVLFLPSNEGEKICLCTSVLVLSTVFL 297
Db 233 PDITVAFIRRLPLFLYTLFLIIPICIGLSFLTVLFLPSNEGEKICLCTSVLVLSTVFL 292
QY 298 VIEEIPSSKVIPIGLIGYVLTMTIFVLSIMVTVPAINIHRSSTNNAMAPLVKIKPL 357
Db 293 LITEIPSTSLVPIGLIGYVLTMTIFVLSIMVTVPAINIHRSSTNNAMAPLVKIKPL 351
QY 358 HTPLKLLCWR-----SHVDRYFTQKE----- 378
Db 352 DIVPRLFWKRSVVKDNCRRILIESMKMANAPRFPWPESPGLIGDIGNOGLSPATPF 411
QY 379 -----ETESGS-----GPKSS----- 389
Db 412 CNRMDTAVETQTCRSPSHKVPDLKTSEVKASPCPSPGSCHPNNSGAPVLKARLSV 471
QY 390 ---RNTLEAALNSIR----- 401
Db 472 QHVPSSQEAAGSIRCSRISIQYCVSODGAASLTESKPTGSPASLKRPSQLPVSDQTS 531
QY 402 -----YITRHKMKENDVREVE 418
Db 532 CKCTCKEPPSPITVLKAGTKAPQHLPLSPALTRAVEGVQYIADHLKAEDTDFSVKE 591
QY 419 DWKFTIAQLDRMLFTFLFVSVIGSLGLFVP 449
Db 592 DWKYAWVIDRFLMFWIIVCLLGTGVGLF 622

RESULT 12
Q9ROW9 PRELIMINARY; PRT; 494 AA.
ID Q9ROW9
AC Q9ROW9
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha6.
GN CHRNA6 OR NICA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Le Novere N.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Marubio L.M., Champetiaux N., Changeux J.P.;
RT "Cloning of the nicotinic acetylcholine receptor subunit alpha6 from
RT mouse brain.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AJ245706; CAB53472.1; -.
DR MGD; MGI:106213; Chna6.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
SQ SEQUENCE 494 AA; 56807 MW; 650E6CD5CFCD745F CRC64;
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Query Match 46.4%; Score 1139; DB 11; Length 494;
Best Local Similarity 46.8%; Pred. No. 5.5e-87;

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Matches 221; Conservative 92; Mismatches 105; Indels 54; Gaps 8;
QY 37 LSEPSIAKHEDSLKDLFQDYERWVREHLNDKIKIFGLAIQSOLVDVDEKNQMTTN 96
Db 24 LFKSGTGCSEBEQLFHLFAHYNRFRFVENVSDPTVHLELAITQLANDEVNQIMETN 83
QY 97 VWLQKQWIDVKLRNPDYGGIKVIRVPSDSWTPDVLFDNADGRF--EGTSTKTIVRY 154
Db 84 LMLRHIMKDYRLRMDPTDYDGIETLRVPADNIWKPDIVLYNNAVGDFQVEG-KTKALLKY 142
QY 155 NGTWTWTPPNKSSCTIDVTFEPDLONCSMKFGSWTYDGSVDIILEDQDVDRDRPD 214
Db 143 DGVIWTWTPALFKSCPMIDITFPFPHQNSLKFGSWTYDKAIDLLILGSKVDNWFWE 202
QY 215 NGEWEIVSATSGKNRTDSCC--WYVYVYTSFVIRKRLFLFTFLIIPICIGLSFLTVLV 272
Db 203 NSEWEIVDASGVKHDIKYNCCEIYTDITYSFYIRRLPMFYTNLIIFCLFISFLTVLV 262
QY 273 YLPNNEGEKICLCTSVLVLSTVFLVLVIBEEIIPSSSKVPIPLIGEYLVFTMIFFVLSIMVT 332
Db 263 YLPSCDCEKVTCLISVLLSLTVFLVLVITETIPSTSLVPLVGEYLLFTMIFFVLSIVTV 322
QY 333 FAINIHRSSTNNAMAPLVKIKPLHTLPLKLLCWRSHVDR----- 372
Db 323 FVLNIHYKTPATH-TMPKWVKTIFLQAPPSILMMRKPLDKTKBAGGVKDPKSHTRKPAKV 381
QY 373 YFTQKEETE-----SGSGPKSRNT-----LEAALNSIRYITR 405
Db 382 KPTRGESKLLKECHCKQSSDIAPGKRSSQOPARWVAENSEHSSDVEDVIESVOFTAE 441
QY 406 HIMKENDVREVEVDWKFTIAQLDRMLFTFLFVSVIGSLGLFV-PVIYKWN 456
Db 442 NMKSHNETNEVEDWKYMAWVDRVFLVWFVFIIVCVFVGLFLOPLGLNTGN 493

RESULT 13
Q9VHH6 PRELIMINARY; PRT; 499 AA.
ID Q9VHH6
AC Q9VHH6;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha 3 subunit.
GN CHRNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Brain;
RT "Mouse neuronal nicotinic acetyl choline receptor alpha 3 subunit
RT mRNA.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF459029; AAL58471.1; -.
DR MGD; MGI:87887; Chna3.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
SQ SEQUENCE 499 AA; 57125 MW; D21650F6A6D7C14B CRC64;
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Query Match 44.7%; Score 1097.5; DB 11; Length 499;
Best Local Similarity 43.2%; Pred. No. 1.7e-83;
Matches 217; Conservative 97; Mismatches 109; Indels 79; Gaps 7;

Qy 8 PRALRLLLLVQVAGRCGLAGAGGAQAGLSEPSSTAKHEDSLKDLFQDYERWVRVEH 67
Db 7 PPPLSMLMLVLM-----LLPVASASEAHLRFQYLFEDYNEIIRVAN 49

Qy 68 LNDKIKIKFGLAISQVLDVDEKNQMTNVLKQEWIDVKLRWNPDDYGGIKVIRVPSDS 127
Db 50 VSHPVIIQFEVSNLSQVQVDEVNQIMETNLWLKQIWNQYKWKPSDYQGVEMRVPABK 109

Qy 128 VMTPDIVLFNADGRPE-GTSTKTVIRYNGTVTWTPPANYSKSTCTIDVTFPPDLQNCMS 186
Db 110 IKRPDIVLYNNADGDFQVDDKTKALLKYTGCVTWIPPAIFKSSCKIDVTYFPFDYQNCMTM 169

Qy 187 KFGSWTYDGSQVDIILEDQDDVKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPYVTVYSF 244
Db 170 KFGSWSYDKAKIDLVIGSSMNLKDYWESGEWAIKAPGYKHEIKYNCCEIYQDITYSL 229

Qy 245 VIKRLPLFYTLFLIIPCLISFLTVLVFVLPSPDCEKVTLCISVLLSLTVFLVITETIP 289
Db 305 SSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNAAPLVKRFILHTLPKLL 364
Db 290 STSLVPLIGEYLLFTMIFVTLISIVTVFVLNVHYRTPTTH-TMPTWVKAFLNLLPRVM 348

Qy 365 CMRSHVDVRYFTQKEETESGSGPK----- 387
Db 349 -----FMTPTSTEE-DAPKTRNFYGAELSNLNCFSRADSKSCKEGYLCQDGTGCGYCHRRVRKISN 408

Qy 381 ESGSGPKSSN-----TLEAALNSIRYITRHKENDVREVVEDWKFTAOV 426
Db 409 FSNALTRSSSESVDVLSLSALSPETKEAIQSVKYIAENKQAQNVAKETQDDWKYVAMV 468

Qy 427 LDRMFLWTLFVSVISGLFLV 448
Db 469 IDRIFLWVFLVLCILGTAGLFL 490

RESULT 14
Q8B4G9 PRELIMINARY; PRT; 499 AA.
AC Q8B4G9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 3 subunit.
GN CHRNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/21bg; TISSUE=Adrenal gland;
RA Lautner M.A., Scitzel J.A.;
RT "Cloning of mouse nicotinic acetylcholine receptor alpha 3 subunit cDNA."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion, and Eye;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF472588; AAL84757.1; --
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DR EMBL; AK051730; BAC34740.1; --
DR EMBL; AK053497; BAC35404.1; --
DR MGD; MGI:87887; Chrna3.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR006201; Neur_chan_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC_1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 499 AA; 57109 MW; 721650B3F38D00FD CRC64;

Query Match 44.7%; Score 1097.5; DB 11; Length 499;
Best Local Similarity 42.5%; Pred. No. 1.7e-83;
Matches 217; Conservative 95; Mismatches 102; Indels 97; Gaps 8;

Qy 8 PRALRLLLLVQVAGRCGLAGAGGAQAGLSEPSSTAKHEDSLKDLFQDYERWVRVEH 67
Db 7 PPPLSMLMLVLM-----LLPVASASEAHLRFQYLFEDYNEIIRVAN 49

Qy 68 LNDKIKIKFGLAISQVLDVDEKNQMTNVLKQEWIDVKLRWNPDDYGGIKVIRVPSDS 127
Db 50 VSHPVIIQFEVSNLSQVQVDEVNQIMETNLWLKQIWNQYKWKPSDYQGVEMRVPABK 109

Qy 128 VMTPDIVLFNADGRPE-GTSTKTVIRYNGTVTWTPPANYSKSTCTIDVTFPPDLQNCMS 186
Db 110 IKRPDIVLYNNADGDFQVDDKTKALLKYTGCVTWIPPAIFKSSCKIDVTYFPFDYQNCMTM 169

Qy 187 KFGSWTYDGSQVDIILEDQDDVKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPYVTVYSF 244
Db 170 KFGSWSYDKAKIDLVIGSSMNLKDYWESGEWAIKAPGYKHEIKYNCCEIYQDITYSL 229

Qy 245 VIKRLPLFYTLFLIIPCLISFLTVLVFVLPSPDCEKVTLCISVLLSLTVFLVITETIP 289
Db 305 SSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNAAPLVKRFILHTLPKLL 364
Db 290 STSLVPLIGEYLLFTMIFVTLISIVTVFVLNVHYRTPTTH-TMPTWVKAFLNLLPRVM 348

Qy 365 CMRSHVDVRYFTQKEETESGSGPK----- 387
Db 349 -----FMTPTSTEE-DAPKTRNFYGAELSNLNCFSRADSKSCKEGYLCQDGTGCGYC 399

Qy 388 -----SSRNTLEA-----ALNSIRYITRHKENDVREV 417
Db 400 HHRVXISNFSANLTRSSSESVDVLSLSALSPETKEAIQSVKYIAENKQAQNVAKETQ 459

Qy 418 EDWKFTAOVLDNRMLWTLFVSVISGLFLV 448
Db 460 DDKYVAMVIDRIFLWVFLVLCILGTAGLFL 490

RESULT 15
Q8B4V4 PRELIMINARY; PRT; 504 AA.
AC Q8B4V4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuronal NICOTINIC acetylcholine receptor alpha 3 subunit.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
```


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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 18:47:38 ; Search time 24 Seconds
(without alignments)
917.021 Million cell updates/sec

Title: US-09-703-951A-8

Perfect score: 2456

Sequence: 1 MAARGSPRALRLLLLVQLV.....PVIYKANILIPVHGNANK 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2451	99.8	468	1 ACH5 HUMAN	P30532 homo sapien
2	2148.5	87.5	452	1 ACH5_RAT	P20420 rattus norv
3	2034	82.8	454	1 ACH5_CHICK	P26152 gallus gall
4	1586	64.6	458	1 ACHO HUMAN	Q05901 homo sapien
5	1579.5	64.3	462	1 ACHO CARAU	P13908 carassius a
6	1568.5	63.9	455	1 ACHO CHICK	P43679 gallus gall
7	1534	62.5	464	1 ACHO_RAT	P12391 rattus norv
8	1531	62.3	466	1 ACHP_CARAU	P18257 carassius a
9	1201.5	48.9	529	1 ACH2 HUMAN	Q15822 homo sapien
10	1179	48.0	511	1 ACH2_RAT	P12389 rattus norv
11	1166.5	47.5	528	1 ACH2 CHICK	P09480 gallus gall
12	1157.5	47.1	627	1 ACH4 HUMAN	P43681 homo sapien
13	1143	46.5	512	1 ACH4 CARAU	P18845 carassius a
14	1142.5	46.5	630	1 ACH4_RAT	P09483 rattus norv
15	1139	46.4	493	1 ACH6_RAT	P13143 rattus norv
16	1135	46.2	494	1 ACH6 HUMAN	Q15825 homo sapien
17	1129.5	46.0	622	1 ACH4 CHICK	P09482 gallus gall
18	1119.5	45.6	494	1 ACH6 CHICK	P49581 gallus gall
19	1116.5	45.5	495	1 ACH3 BOVIN	Q07263 bos taurus
20	1114	45.4	496	1 ACH3_CHICK	P09481 gallus gall
21	1112	45.3	503	1 ACH3 HUMAN	P32297 homo sapien
22	1096.5	44.6	499	1 ACH3_RAT	P04757 rattus norv
23	1028.5	41.9	498	1 ACHP HUMAN	P30926 homo sapien
24	1025.5	41.8	567	1 ACH1 DROME	P09478 drosophila
25	1024	41.7	516	1 ACH1_MANSE	P91766 manduca sex
26	1020.5	41.6	456	1 ACHA_CHICK	P09479 gallus gall
27	1020	41.5	519	1 ACHA DROME	P25162 drosophila
28	1019.5	41.5	457	1 ACHA_MOUSE	P04756 mus musculu
29	1016	41.4	495	1 ACHP_RAT	P12392 rattus norv
30	1012	41.2	457	1 ACHA BOVIN	P02709 bos taurus
31	1009.5	41.1	457	1 ACHA_RAT	P25108 rattus norv
32	1000	40.7	557	1 ACH1_SCHGR	P23414 schistosom
33	998	40.6	461	1 ACHA_TORMA	P02711 torpedo mar

RESULT 1

ACH5_HUMAN

ID ACH5_HUMAN STANDARD; PRT; 468 AA.

AC P30532; Q15824; Q99554;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-5 chain precursor.

GN CHRNA5 OR NACHRA5

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=92179225; PubMed=1542648;

RA Chini B., Clementi F., Hukovic N., Sher E.;

RT "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic receptor subunit gene are expressed in neuronal and nonneuronal human cell lines";

RL Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=97062879; PubMed=8906617;

RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Johnson E.C., Velicellebi G., Harpold M.M.;

RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta

2-beta 4 nicotinic acetylcholine receptor subunits and functional

expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and

beta 4 subunits";

RL J. Mol. Neurosci. 7:217-228(1996).

RN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=97162233; PubMed=9009220;

RA Groot Kormelink P.J., Luyten W.H.M.L.;

RT "Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32";

RL FEBS Lett. 400:309-314(1997).

RN (4)

RP SEQUENCE FROM N.A.

RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,

Tenchini M.L.;

RT "Characterization of the genomic structure of human nicotinic

acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of

two novel introns in the 3' untranslated region of CHRNA3 and of a

tail-to-tail overlap between CHRNA3 and CHRNA5";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

MEMBRANE.

CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT

TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

ALIGNMENTS

P19370 carassius a
P02708 homo sapien
P05377 xenopus lae
P17644 drosophila
P02710 torpedo cal
P17787 homo sapien
P12390 rattus norv
P23456 xenopus lae
P09484 gallus gall
P26153 gallus gall
Q98880 brachydanio
Q23022 caenorhabdi

34 994 40.5 459 1 ACHN_CARAU
35 991.5 40.4 482 1 ACHA_HUMAN
36 991 40.4 457 1 ACH2_XENLA
37 990 40.3 576 1 ACH2_DROME
38 987 40.2 461 1 ACHA_TORCA
39 984 40.1 502 1 ACHN_HUMAN
40 982.5 40.0 500 1 ACHN_RAT
41 977.5 39.8 457 1 ACH1_XENLA
42 977.5 39.8 491 1 ACHN_CHICK
43 972.5 39.6 470 1 ACHP_CHICK
44 972 39.6 456 1 ACHA_BRARE
45 926 37.7 511 1 ACH5_CABEL

J. Biol. Chem. 265:17560-17567(1990).

-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.

-!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND THREE NON-ALPHA CHAINS.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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	Matches	3/8; Conservative	30; Mismatches	35; Indels	0; Gaps	0
QY	25	GLAGAAGGAQRGLSPSSIAKHEDSLIKDLFDQYERWVRPVEHLNDKIKIKFGLAISQLV	84			
DB	11	GAGPAARAQAQGVSEPSFVAKSEDRLFKHLFEDYQRWVRPVEHLNDTIKIKFGLAISQLV	70			
QY	85	VDVEKNQLMTTNWLKQEWIDVKLRWNPDDYGGIKIVRPSPSVWTPDVLVFNADGRPE	144			
DB	71	VDVEKNQLMTTNWLKQEWIHVKLRWNPEDYAGITSIRVPSPSIWTPDVLVFNADGRPE	130			
QY	145	GTSTKTVIRYNGTGTWTPPANKYKSSCTIDVTFFPDLQNCMKFGSWTVDGGSQVDIILED	204			
DB	131	GTSTKTVIRYKIDGTIATWTPVNTKSSCTIDVTFFPDLQNCMKFGSWTVDGGSQVDIILED	190			
QY	205	QVDVKRDPFDNGEWEIVSATGSKGNRTDCWCWVPVYTSYFVIRKRLPFTLFLIIPCIGL	264			
DB	191	YEVDVKRDPFDNGEWEIVTATGSKGNRTDCWCWVPVYTSYFIIRRLPFTLFLIIPCIGL	250			
QY	265	SFLTVLVFLVPLPNEGEKICLCTSVLVSFLTFLVLVTEIIPSSKVIPLTGEVLVFTMIFV	324			
DB	251	SFLTVLVFLVPLPNEAEKISLCTSVLVSFLTFLVLVTEIIPSSKVIPLTGEVLVFTMIFV	310			
QY	325	TLSIVMTVPAIINHRSSSTHNAAPLVRKIFLHTLPKLLCMRSHVDYFTFOKEETESGS	384			

RESULT 5					
ID	ACHO_CARAU	STANDARD;	PRT;	462 AA.	
AC	P13908;				
DT	01-JAN-1990	(Rel. 13, Created)			
DT	01-JAN-1990	(Rel. 13, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, non-alpha-2 chain precursor				
DE	(GFN-alpha-2).				
DE	Carassius auratus (Goldfish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Carassius.				
ON	NCBI_TaxId=7957;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Retina;				
RC	MEDLINE=89139580; PubMed=2465296;				
RX	Cauley K., Agranoff B.W., Goldman D.J.;				
RA	"Identification of a novel nicotinic acetylcholine receptor				
RT	structural subunit expressed in goldfish retina.";				
RT	J. Cell Biol. 108:637-645(1989).				
RL	-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN				
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND				
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA				
CC	MEMBRANE.				
CC	-!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT				
CC	TYPE OF SUBUNITS: ALPHA AND BETA.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement [See http://www.isb-sib.ch/announce				
CC	or send an email to license@isb-sib.ch].				
CC	-----				
CC	EMBL; X14786; CAA32888.1; -.				
DR	PIR; S06893; S06893.				
DR	InterPro; IPR006029; Neu channel memb.				
DR	InterPro; IPR006202; Neur_chan_LED.				
DR	InterPro; IPR006201; Neur_channel.				
DR	Pfam; PF02931; Neur_chan_LBD; 1.				
DR	Pfam; PF02932; Neur_chan memb; 1.				
DR	PRINTS; PR00252; NRIONCHANEL.				
DR	TIGRFAMS; TIGR00860; LIC; 1.				
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.				
KW	Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;				
FT	Transmembrane; Multigene family.				
FW	SIGNAL				
FT	CHAIN	31	462		
FT				NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,	
FT					
FT					
FT	DOMAIN	31	234		
FT	TRANSMEM	235	259		
FT	TRANSMEM	267	284		
FT	TRANSMEM	301	322		
FT	DOMAIN	323	428		
FT	TRANSMEM	429	446		
FT	DISULFD	155	169		
FT	CARBOHYD	53	53		
FT				BY SIMILARITY.	
FT				N-LINKED (GLCNAC...) (POTENTIAL).	

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: RELATIVELY ABUNDANT IN THE DEVELOPING RETINA
 CC AND IN THE TRIGEMINAL GANGLION.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; X83739; CAB59814.1; --
 DR PIR; A55972; A55972.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_LBD; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 455 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT BETA-3 CHAIN.
 FT DOMAIN 21 229 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 230 254 POTENTIAL.
 FT TRANSMEM 262 279 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 425 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 426 444 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 52276 MW; 3D7A7AFA77D8511A CRC64;

 Query Match 63.98; Score 1568.5; DB 1; Length 455;
 Best Local Similarity 67.6%; Pred. No. 7e-122;
 Matches 292; Conservative 61; Mismatches 62; Indels 17; Gaps 3;

 QY 42 SIAKHEDSLKDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKNQMTTNWLKQ 101
 DB 21 SVVENEALLRHFLFQGYQKWRVPVENSNDIKVLFGLKISQLVDVDEKNQMTTNWLKQ 80
 QY 102 EWIDVLRWNPDDYGGIKVIRVPSDSVWTPDVLFDNADGRFEGT-STKTVIRYNGVTW 160
 DB 81 EWMHDKLSWNPDEYGGITAIRVPSDSLWLPDVLFDNADGRFEGSLMTKAIVKYNQVQW 140
 QY 161 TPANYKSSCTIDVTFPPFDLONCSMKFGSWTDGSOVDLLEDODVDKDFPDNGWEI 220
 DB 141 MPPASYKSSCTMELTFPPFDLONCSMKFGSWTDGSMVDLILVDENVDTKDFPDNGWEI 200
 QY 221 VSGTSGKNTDSCWYPTYSYVIRKRLPLFTLFIICIGLSFTLVLFVLPSPNEGE 280
 DB 201 LNAKGMKGNKRGDGLYSYPTYSYVIRKRLPLFTLFIICIGLSFTLVLFVLPSPDEGE 260
 QY 281 KICLCTSVLSVTLVFLVIEEIIIPSSSKVPIIGELVLTFTIMFTVLSIMVTVFAINHHR 340
 DB 261 KLSLSTSVLSVTLVFLVIEEIIIPSSSKVPIIGELVLTFTIMFTVLSIIVTVFVNVHR 320
 QY 341 SSSTHNAMAPLVKIFLHTLPLKLCMRSHVDYR-FTQKEETE-----SGS 384
 DB 321 SSATYHPMAPVWRLFLQKLPRLCLCMKGVHDYRFSFSDTEETKTLKSLPKGKHQKQAKD 380
 QY 385 GPKSSRRTLAALNSIRYITRHLMKENDREVWEDKFIQALDRMFLWTFVLSIVGSL 444
 DB 381 GEKVVIATFLKADSIIRYISRHVKKDAFIRQVQVDKFWFAQVLDRIPLWLFVLSVTVGSV 440
 QY 445 GLFVPIYIKWAN 456
 : : : : :

Db 441 LIPTPALQMWLN 452
 RESULT 7
 ACHO RAT STANDARD; PRT; 464 AA.
 AC P12391;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, beta-3 chain precursor.
 GN CHRN3 OR ACRB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89197926; PubMed=2703489;
 RX Deneris E.S., Boulter J., Swanson L.W., Patrick J., Heinemann S.F.;
 RT "Beta 3: a new member of nicotinic acetylcholine receptor gene family
 is expressed in brain.";
 RL J. Biol. Chem. 264:6268-6272(1989).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPES OF SUBUNITS: ALPHA AND BETA.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC ENBL; J04636; AAC28887.1; --
 DR PIR; A33523; A33523.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_LBD; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 464 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT BETA-3 CHAIN.
 FT DOMAIN 31 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 263 POTENTIAL.
 FT TRANSMEM 271 288 POTENTIAL.
 FT TRANSMEM 305 326 POTENTIAL.
 FT DOMAIN 327 434 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 435 453 POTENTIAL.
 FT DISULFID 159 173 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 464 AA; 53261 MW; 5D3B1F7DB934D1D8 CRC64;

 Query Match 62.5%; Score 1534; DB 1; Length 464;
 Best Local Similarity 65.1%; Pred. No. 5.1e-119;
 Matches 286; Conservative 71; Mismatches 62; Indels 20; Gaps 3;

 QY 33 AQRLSEPSISIAKHEDSLKDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKNQ 92
 DB 24 ATAGL---SSVAEHEDALLRHFLFQGYQKWRVPVLSNDSIDIKVYFGLKISQLVDVDEKNQ 80
 : : : : :

QY 93 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTV 151
 Db 81 MTTNVLKQEWTDQKLRNPEYGGINSIKVPSLSLWLPDVLVFNADGRFEGSLMTKAI 140
 QY 152 TRYNGTWTTPANKSSCTIDVTFPPDLQNSMKFGSWTYDGSVDLILDDQVDKRD 211
 Db 141 VKSSGTVSTPASPSSCTMDVTFPPDRQNSMKFGSWTYDGTWDLILNENVDKRD 200
 QY 212 PFDNGEIVSAGSGNRTDCCWYVYTSFVKIRLPLFLFTLFIIPICIGLSFLTVLV 271
 Db 201 PFDNGEIVLNAKMGKNGRREGFYSPFYTSFVLRLPLFLFTLFIIPICIGLSFLTVLV 260
 QY 272 FYLPNSGEKICLTSVLSVLTFLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVTLISMT 331
 Db 261 FYLPNSGEKICLTSVLSVLTFLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVTLISMT 320
 QY 332 VFAINIHRSSTHNAAPLVKIRLHTLPKLLCMRSHVDY-----FT 375
 Db 331 VFAINIHRSSTHNAAPLVKIRLHTLPKLLCMRSHVDY-----FT 375
 QY 376 QKEETESGPKSSNTLEAALNSIRYITRHKENDVREVEDWKFAQVLDRLMFLWTF 435
 Db 381 KRKQTPASDGERVLVAFLEKASESIRYISRHVKKEHFISQVVDWKFAQVLDRLMFLWTF 440
 QY 436 LFVSVGSLGLFVPIYKW 454
 Db 441 LIASVLGSLIFIPALKMW 459

RESULT 8

ACHP_CARAU STANDARD; PRT; 466 AA.
 AC P18257;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, non-alpha-3 chain precursor (GN-alpha-3).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Retina;
 RX MEDLINE=90155434; PubMed=2303867;
 RA Cauley E.A., Agronoff B.W., Goldman D.J.;
 RT "Multiple nicotinic acetylcholine receptor genes are expressed in goldfish retina and tectum."
 RL J. Neurosci. 10:670-683(1990).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: RETINA, TECTUM AND BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 DR EMBL; M29529; AAA49167.1; -;
 DR PIR; S16333; S16333.
 DR InterPro; IPR006029; Neu_channel_membr.

DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEURONAL_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FT Transmembrane; Multigene family.
 FT SIGNAL 1 28
 CHAIN 29 466
 FT DOMAIN 29 235
 FT TRANSMEM 236 260
 FT TRANSMEM 268 285
 FT TRANSMEM 302 323
 FT DOMAIN 324 438
 FT TRANSMEM 439 456
 FT DISULFID 156 170
 FT CARBOHYD 54 54
 FT CARBOHYD 141 141
 FT CARBOHYD 169 169
 FT CARBOHYD 208 208
 SQ SEQUENCE 466 AA; 53801 MW; 3EED8C870CC955F8 CRC64;

NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 NON-ALPHA-3 CHAIN.
 EXTRACELLULAR.

CYTOPLASMIC.

BY SIMILARITY.
 N-LINKED (GLCNAC. .) (POTENTIAL).
 N-LINKED (GLCNAC. .) (POTENTIAL).
 N-LINKED (GLCNAC. .) (PROBABLE).
 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 62.3%; Score 1531; DB 1; Length 466;
 Best Local Similarity 64.8%; Pred. No. 9e-119;
 Matches 283; Conservative 63; Mismatches 67; Indels 24; Gaps 3;

QY 42 SIAGHEDSLKDLFDQYERWVRVPEHLNDKIKIFGLAISQVVDVDEKQMLTTNVLWKQ 101
 Db 27 SLAEMEDTLRLNFRGQKWRPILHANDTITVRFLKISQVVDVDEKQMLTTNVLWKQ 86
 QY 102 EWIDVLRNPDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTVIRYNGTVTW 160
 Db 87 EWTYKLRNPDYGGITSRVPSSETIWLDPDIVENADGRFEGSLMTKAIVRFGTITMW 146
 QY 161 TPPANYKSSCTIDVTFPPDLQNSMKFGSWTYDGSQVDIILEDDQVDKRDFFDNGEWEL 220
 Db 147 TPPASYKSSCTMDVTFPPDRQNSMKFGSWTYDGTWDLTLDDAYVDRKDFDNGEWEL 206
 QY 221 VSATSGKGNRTDSCWYVYTSFVKIRLPLFLFTLFIIPICIGLSFLTVLVFPLPSNEGE 280
 Db 207 LNATGQSGRRDGIYSYVYTSFVKIRLPLFLFTLFIIPICIGLSFLTVLVFPLPSDEGE 266
 QY 281 KICLCSTVLSVLTFLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVTLISMTVFAINIHHR 340
 Db 267 KLLSTSVLSVLTFLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVTLISMTVFAINIHHR 326
 QY 341 SSSTHNAAPLVKIRLHTLPKLLCMRSHVDY-----FTQKEETES 382
 Db 327 SSATYHPAPWVKSFLQRLPRLLCMGHTDRYQYDIELRSPKRMKQKQKSGGG 386
 QY 383 GSGPKSSRN-----TLEAALNSIRYITRHKENDVREVEDWKFAQVLDRLMFLWTF 437
 Db 387 RGGLKEDENQAWIALEKATHSVYISRHVKKEHFIREVQDVKFAQVLDRLMFLWTF 446
 QY 438 VSIIVGSLGLFVPIYKW 454
 Db 447 ASVLGTLITFTPALHMY 463

RESULT 9

ACH2_HUMAN
 ID ACH2_HUMAN STANDARD; PRT; 529 AA.
 AC Q15822; Q9HQA03;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
 GN CHRNA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```

274 QY LPSNGEKICICTSVLSVLTIVELLVTEETIIPSSSKVPIPLIGEVLVTMTIIVTISIMVTVF 333
275 QY LPSNGEKICICTSVLSVLTIVELLVTEETIIPSSSKVPIPLIGEVLVTMTIIVTISIMVTVF 333
266 DB LPSECEGKITLCISVLLSLTVFLLLTETIIPSTSLVIPLIGEVLVTMTIIVTISIVTVF 325
267 DB LPSECEGKITLCISVLLSLTVFLLLTETIIPSTSLVIPLIGEVLVTMTIIVTISIVTVF 325
334 QY ALNIHRSRSTHNAMAPVRKIFLHTLPKLLCWRSHV----- 370
335 QY ALNIHRSRSTHNAMAPVRKIFLHTLPKLLCWRSHV----- 370
326 DB VLNVHRSRSTHN-HPNVTWVALLGRVPRFLMMNRPLPPMELHGSDDLKPSYHWLETN 384
327 DB VLNVHRSRSTHN-HPNVTWVALLGRVPRFLMMNRPLPPMELHGSDDLKPSYHWLETN 384
371 QY -----DRYFTQKETEESGSG-----PKSSRNTL----- 393
372 QY -----DRYFTQKETEESGSG-----PKSSRNTL----- 393
385 DB MDAGERETEETEEEDENICVACGLPDSGVLVYGHGGLHLRAMEPETKTPSOASEILL 444
386 DB MDAGERETEETEEEDENICVACGLPDSGVLVYGHGGLHLRAMEPETKTPSOASEILL 444
394 QY ----EALNISRYIITHINKENDREVVEDKFIQVIAQVLDRLMPLWTFLFVSIIVCSGLGFVP 449
395 QY ----EALNISRYIITHINKENDREVVEDKFIQVIAQVLDRLMPLWTFLFVSIIVCSGLGFVP 449
445 DB SPOIQKALEGVHYIADRLSESDADSSVKEDWKYVAMVVDRIFLWLFIIVCFGLTIGLFLP 504
446 DB SPOIQKALEGVHYIADRLSESDADSSVKEDWKYVAMVVDRIFLWLFIIVCFGLTIGLFLP 504

RESULT 11
ACH2_CHICK
ID ACH2_CHICK STANDARD; PRT; 528 AA.
AC P09480;
AC P09480;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
OS Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RN [1]
RP TISSUE=Brain;
RC MEDLINE=88283624; PubMed=3267226;
RX Nef P., Onysysz C., Alliod C., Couturier S., Ballivet M.;
RA "Genes expressed in the brain define three distinct neuronal
RT nicotinic acetylcholine receptors."
RL EMBO J. 7:595-601(1988).
CC -! FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -! SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC THREE NON-ALPHA CHAINS.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07339; CAB59645.1; --
CC EMBL; X07340; CAB59645.1; JOINED.
CC EMBL; X07341; CAB59645.1; JOINED.
CC EMBL; X07342; CAB59645.1; JOINED.
CC EMBL; X07343; CAB59645.1; JOINED.
CC EMBL; X07344; CAB59645.1; JOINED.
CC EMBL; X07345; CAB59645.1; --
CC EMBL; X07346; CAB59645.1; --
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CC EMBL; X07453; CAB59645.1; --
CC EMBL; X07454; CAB59645.1; --
CC EMBL; X07455; CAB59645.1; --
CC EMBL; X07456; CAB59645.1; --
CC EMBL; X07457; CAB59645.1; --
CC EMBL; X07458; CAB59645.1; --
CC EMBL; X0
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RL Nucleic Acids Res. 18:5293-5293 (1990).

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT

CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC

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CC

DR EMBL; X54051; CAA37985.1; -

DR PIR; S11230; B37014.

DR InterPro; IPR006029; Neu channel memb.

DR InterPro; IPR006202; Neu_chan_LBD.

DR InterPro; IPR006201; Neu_chan_LBD.

DR Pfam; PF02931; Neu_chan_LBD; 1.

DR Pfam; PF02932; Neu_chan_LBD; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR TIGR; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 512 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,

FT DOMAIN 24 232 ALPHA-3 CHAIN.

FT TRANSMEM 233 257 EXTRACELLULAR.

FT TRANSMEM 265 283 CYTOPLASMIC.

FT TRANSMEM 299 320

FT DOMAIN 321 485

FT TRANSMEM 486 505

FT DISULFID 151 165

FT DISULFID 215 216

FT CARBOHYD 47 47

FT CARBOHYD 164 164

SQ SEQUENCE 512 AA; 58095 MW; 8D2F63E37CE9077 CRC64;

Query Match 46.5%; Score 1143; DB 1; Length 512;

Best Local Similarity 43.7%; Pred. No. 1.1e-86;

Matches 229; Conservative 90; Mismatches 109; Indels 96; Gaps 8;

QY 6 SGPRLRLLLVLVACRCGLAGGAAGGAGRGGLSEPSIAKHEDSLKDLFDYERVRVPV 65

DB 3 SASRITLFFLLTVLTQEC-----LS-----SKGEDRLPRLFRFYNQFIRPV 45

QY 66 EHLNDKIKIFGLAISQDVDEKNQMLTNTNVLKQEWIDKLRNPDGCGIKVRVPS 125

DB 46 ENVSDDPTVFEVSISQLVKVDVQMEINLWLRHNDYKWLPAEFDGIEFIRVPS 105

QY 126 DSVWTPDIVLFDNADGRF-EGTSTKTVIRNGTVTPPPANYKSSCTIDVTFPFDLQNC 184

DB 106 NKIRPDIIVLYNNAVGDFVEDKTKALKYDGTITVTPVPAIFKSSCPMDITYPPFDYQNC 165

QY 185 SMKFGSTYDGSQVDITLQDDVDKDPDFDNGEWEIVSATGSGNRTDSC--WYPVVTV 242

DB 166 SMKFGSTYDQAKIDLVLSGKNLQDFWESGEWEIIDAFYKHDIKYNCCEIYPDITY 225

QY 243 SFVKIRLPFLFTLPIICGLSLTLVLVFLYPSNEGEKICLCTSLVLSVLTFLVLTVEEI 302

DB 226 SFYIRLPFLFTLPIICGLSLTLVLVFLYPSNEGEKICLCTSLVLSVLTFLVLTVEEI 285

QY 303 IPSSKVIPIGELVFTMIFVLSIMVTVPAINHHRSSSTNNAPLVKFIPLHTLPK 362

DB 286 IPSTSLVPIGELVFTMIFVLSIVITVFLNVHVTMTMTH-TMPSWVTVFLRALPR 344

QY 363 LLCMRSHVDYRFTQ----- 376

DB 345 VMLRRPIDLSSSGKGCGEAGSSGTGGGAEKGMKSSASQCGAMNSLSPGEGKAAL 404

QY 377 -----KEETESGSGPKSSRNTLEA-----ALNSTRYITRHM 408

DB 405 EGGKGGCPCHPIKEAIEGDCGVSRQLTPQAINTVTVFWSVPEIKQAIESVKYIAENMR 464

QY 409 KENDREVVEDMKFTAQVLDRLMFLTFVSLVGSGLFV-PVI 451

DB 465 SRNKAKEVEDDKWYVAMVDIRFLWVFLVGVGLGLFLQPLI 508

RESULT 14

ACH4_RAT

ID ACHA_RAT STANDARD; PRT; 630 AA.

AC P09483; O35769;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-4 chain precursor.

GN CHRNA4 OR ACRA4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus, and Hypothalamus;

RX MEDLINE=87159533; PubMed=3829125;

RA Goldman D.J., Deneris E.S., Luyten W., Kochhar A., Patrick J.,

RA Heinemann S.F.;

RT "Members of a nicotinic acetylcholine receptor gene family are

RT expressed in different regions of the mammalian central nervous

RT system.";

RL Cell 48:965-973 (1987).

RN [2]

RP REVISIONS.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Hartley M., Goldman D.J., Heinemann S.F.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Boulter J., Deneris E.S., Evans K., Heinemann S.F.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP PARTIAL SEQUENCE OF 31-47.

RX MEDLINE=87276531; PubMed=3609304;

RA Whiting P., Esch F., Shimasaki S., Lindstrom J.;

RT "Neuronal nicotinic acetylcholine receptor beta-subunit is coded for

RT by the cDNA clone alpha 4.";

RL FEBS Lett. 219:459-463 (1987).

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES

CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-4 SUBUNIT CAN BE

CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Alpha-4-1; Sequence=Displayed;

CC IsoId=P09483-1; Name=Alpha-4-2;

CC IsoId=P09483-2; Sequence=VSP_000074;

CC -1- TISSUE SPECIFICITY: IN VARIOUS REGIONS OF THE CENTRAL NERVOUS

CC SYSTEM.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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[illegible]

Db	352	LDIVPRLLFWKRP	SVWDCNCRRLIESMHKMANAP	FRFWPEPVGEPGILLSDICNOGLSPAPT	411
Qy	375	-----	-----	-----	374
Db	412	FCNPDTDAVETQ	TCRSPPLEVDPDKTSEVEKASPCSPGSGCSPKPPKSSSGAPMLIKARSL	471	
Qy	375	-----	-----	-----	395
Db	472	SVQHVPSSQEAADG	IRCSRSIQYCVSODGAASLADSKPTSSPTSLKARPSQLPVSQQA	531	
Qy	396	-----	-----	-----	416
Db	532	SPCKCTCKERSPV	PTVTLKAGGTAKPQHLPLSPALTRAVEGVQYIADHLKAEDTDFSV	591	
Qy	417	VEDWKFTAQVLD	RMFLWTLFLFVSIVSGSLGFVP	449	
Db	592	KEDWKYAMVIDR	IFLWFIIVCLGTGVLFLP	624	

RESULT 15

	ACH6_RAT	STANDARD;	PRT; 493 AA.
AC	P43143;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Neuronal acetylcholine receptor protein, alpha-6 chain precursor.		
GN	CHRNA6 OR ACRNA6.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Boulter J.;		
RL	Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).		
EMBL;	L08227; AAA41674.1; ..		
DR	InterPro; IPR006029; Neu channel memb.		
DR	InterPro; IPR006202; Neur_chan_LBD.		
DR	InterPro; IPR006201; Neur_channel.		
DR	Pfam; PF02931; Neur_chan_LBD; 1.		
DR	Pfam; PF02932; Neur_chan_memb; 1.		
DR	PRINTS; PR00252; NRIONCHANNEL.		
DR	TIGRFAMs; TIGR00860; LIC; 1.		
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.		
KW	Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.		
FT	SIGNAL	1 30	BY SIMILARITY.
FT	CHAIN	31 493	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT			ALPHA-6 CHAIN. (POTENTIAL).
FT	DOMAIN	31 240	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	241 265	POTENTIAL.
FT	TRANSMEM	272 290	POTENTIAL.
FT	TRANSMEM	306 327	POTENTIAL.
FT	DOMAIN	328 464	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	465 484	POTENTIAL.
FT	DISULFID	158 172	BY SIMILARITY.
FT	DISULFID	222 223	ASSOCIATED WITH RECEPTOR ACTIVATION

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 20:50:42 ; Search time 37 Seconds
(without alignments)
1216.404 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVLQV.....PVIYKANILIPVHIGNANK 468
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2365	96.3	468	2 A38223	nicotinic acetylch
2	2148.5	87.5	452	2 A35721	nicotinic acetylch
3	2047	83.3	454	2 B3218	nicotinic acetylch
4	1579.5	64.3	462	2 S0893	nicotinic acetylch
5	1574.5	64.1	455	2 S5116	nicotinic acetylch
6	1568.5	63.9	455	2 A55972	nicotinic acetylch
7	1534.5	62.5	423	2 I38056	nicotinic acetylch
8	1534	62.5	464	2 A33523	nicotinic acetylch
9	1531	62.3	466	2 S16333	nicotinic acetylch
10	1184	48.2	511	2 A40110	nicotinic acetylch
11	1166.5	47.5	528	1 ACCH4N	nicotinic acetylch
12	1157.5	47.1	627	2 JCA021	nicotinic acetylch
13	1145	46.6	625	2 A26456	nicotinic acetylch
14	1143	46.5	512	2 B37014	nicotinic acetylch
15	1133.5	46.2	494	2 T09289	nicotinic acetylch
16	1129.5	46.0	622	1 ACCH4N	nicotinic acetylch
17	1116.5	45.5	495	2 S60589	acetylcholine rece
18	1114.5	45.4	503	2 A53956	nicotinic acetylch
19	1102.5	44.9	502	2 A37040	nicotinic acetylch
20	1096.5	44.6	499	2 A24572	nicotinic acetylch
21	1028.5	41.9	498	2 G02421	nicotinic acetylch
22	1022.5	41.6	567	1 ACFFA1	nicotinic acetylch
23	1020.5	41.6	456	1 ACCH4N	nicotinic acetylch
24	1016.5	41.4	457	2 A24383	nicotinic acetylch
25	1014	41.3	457	1 ACHUA1	nicotinic acetylch
26	1013.5	41.3	445	2 I49458	acetylcholine rece
27	1012	41.2	457	1 ACBOA1	nicotinic acetylch
28	1011	41.2	500	2 S12899	nicotinic acetylch
29	1009.5	41.1	457	2 S13872	nicotinic acetylch

ALIGNMENTS

RESULT 1

A38223
nicotinic acetylcholine receptor alpha-5 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: A38223

R:Chini, B.; Clementi, F.; Hukovic, N.; Sher, E.
Proc. Natl. Acad. Sci. U.S.A. 89, 1572-1576, 1992

A:Title: Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic receptor s

A:Reference number: A38223; MUID:92179225; PMID:1542648

A:Accession: A38223

A:Molecule type: mRNA

A:Residues: 1-468 <CHI>

A:Cross-references: GB:M03712; NID:g177925; PIDN:AA58357.1; PID:g177926

A:Experimental source: IMR32 neuroblastoma cell line

A>Note: sequence extracted from NCBI backbone (NCBI:853377, NCBI:853378)

C:Superfamily: acetylcholine receptor

C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-468/Product: nicotinic acetylcholine receptor alpha-5 chain #status predicted <MAT>

F:251-275/Domain: transmembrane #status predicted <TM1>

F:282-304/Domain: transmembrane #status predicted <TM2>

F:310-335/Domain: transmembrane #status predicted <TM3>

F:422-447/Domain: transmembrane #status predicted <TM4>

F:155,183,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.3%; Score 2365; DB 2; Length 468;

Best Local Similarity 97.0%; Pred. No. 6.9e-187;

Matches 454; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy	1	MAARGSPRALRLLLVLQVAGRCGLAGACGAGRGSLSEPSIAKHEDSLKDLFPDYER	60
Db	1	MAARGSPRALRLLLVLQVAGALRRSRAARRGLSEPSIAKHEDSLKDLFPDYER	60
Qy	61	WVRPVEHLNDKIKIFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV	120
Db	61	WVRPVEHLNDKIKIFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV	120
Qy	121	IRVPSDSVWTPDVLFDNADRGFGSTKTVIRYNGTVTTPPPANYKSSCTIDVTFPPFD	180
Db	121	IRVPSDSVWTPDVLFDNADRGFGSTKTVIRYNGTVTTPPPANYKSSCTIDVTFPPFD	180
Qy	181	LQNCMKFGSWTYDGSQVDIILEDQVDVKRDPFNGWEIVSATGSKGNRTDSCWYPYV	240
Db	181	LQNCMKFGSWTYDGSQVDIILEDQVDVKRDPFNGWEIVSATGSKGNRTDSCWYPYV	240
Qy	241	TYSFVKRLPYTLFLIIPICIGSLFVLVFLPSNAGEKICLCTSVLSLTVFLVLVIE	300
Db	241	TYSFVKRLPYTLFLIIPICIGSLFVLVFLPSNAGEKICLCTSVLSLTVFLVLVIE	300
Qy	301	EIIPSSSKVPIGLIGEVLVFTMIFVTLTSMVTVFAINTIHRSSSTHNAAPLVKIFLHTL	360

QY	161	TPPANYKSSCTTIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDVDRKDFDNGSEWI	220
Db	141	MPASYSKSSCTMELTFPPDRQNCMKFGSWTYDGSWVDLIILVDENVDTKDFDNGSEWI	200
QY	221	VSATSGKGNRTDCCWYPVVTYSFVVKRPLPFLVTLFIIPICIGLSFLTVLVFLPSNEGE	280
Db	201	LNAGKMGKNGKDGLSYFPVTYSFVLRRLPFLVTLFIIPICIGLSFLTVLVFLPSDEGE	260
QY	281	KICLCTSVLVSITVFLLVIEEIIIPSSSKVPIPLIGEYLVFTMIFTVLSIMTVFAINIHR	340
Db	261	KLSLSTSVLVSITVFLVLVIEEIIIPSSSKVPIPLIGEYLLFTMIFTVLSIIVTFVINVHR	320
QY	341	SSSTHNAMAPLVKRIPLHTLPKLLCWRSHVDRY-FTQKEBTE	384
Db	321	SSATYHPMAPLVKRLPFLQKLPRLLCMKGHVDYVSFSDTEKETTLKSKLPQKQKQAKD	380
QY	385	GPKSSRNTLEAALNSIRYITRIHMKENDVREVVDWKPIAQLVDRMPLTFLFVSVISGL	444
Db	381	GBKWIATFEKAADSIYISRHVKDAFIRQVQDMKFAQVLDRIFLMLFLVVSVTGSV	440
QY	445	GLFVPVVIYKWN 456	
Db	441	LIFTPALQMWLN 452	

RESULT 6

A55972

nicotinic acetylcholine receptor beta-3 chain precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jul-2000

C:Accession: A55972

R:Hernandez, M.C.; Erkman, L.; Matter-Sadzinski, L.; Rortocil, T.; Ballivet, M.

J. Biol. Chem. 270, 3224-3233, 1995

A:Title: Characterization of the nicotinic acetylcholine receptor beta3 gene. I

A:Reference number: A55972; MUID:95155414; PMID:7852408

A:Accession: A55972

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <HER>

A:Cross-references: GB:1X8739; NID:96165256; PIDN:CAB59814.1; PID:96165257

C:Superfamily: acetylcholine receptor

C:Keywords: neurotransmitter receptor

Query Match	63.9%;	Score	1568.5;	DB 2;	Length	455;			
Best Local Similarity	67.6%;	Pred. No.	2.7e-121;						
Matches	292;	Conservative	61;	Mismatches	62;	Indels	17;	Gaps	3;

QY	42	STAKHEDSLKDLFDYERWRVPRVHLNDKIKIFGLAISQLVDVDEKQMLMTNVLWKQ	101
Db	21	SVVENEDALLRHLPQYQKWVPVENSNDTIKVLFGKLISQLVDVDEKQMLMTNVLWKQ	80
QY	102	EWIDVKLRNPDYGGIKVIRVPSDSVMTDPDVLFDNADGRFEGT-STKTVIRYINGVTW	160
Db	81	EWMDHKLWNPEYGGITAIRVPSBSLMDPLVLFENADGRFEGSLMTKAIVKYGVVQW	140
QY	161	TPPANYKSSCTTIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDVDRKDFDNGSEWI	220
Db	141	MPASYSKSSCTMELTFPPDRQNCMKFGSWTYDGSWVDLIILVDENVDTKDFDNGSEWI	200
QY	221	VSATSGKGNRTDCCWYPVVTYSFVVKRPLPFLVTLFIIPICIGLSFLTVLVFLPSNEGE	280
Db	201	LNAGKMGKNGKDGLSYFPVTYSFVLRRLPFLVTLFIIPICIGLSFLTVLVFLPSDEGE	260
QY	281	KICLCTSVLVSITVFLLVIEEIIIPSSSKVPIPLIGEYLVFTMIFTVLSIMTVFAINIHR	340
Db	261	KLSLSTSVLVSITVFLVLVIEEIIIPSSSKVPIPLIGEYLLFTMIFTVLSIIVTFVINVHR	320
QY	341	SSSTHNAMAPLVKRIPLHTLPKLLCWRSHVDRY-FTQKEBTE	384
Db	321	SSATYHPMAPLVKRLPFLQKLPRLLCMKGHVDYVSFSDTEKETTLKSKLPQKQKQAKD	380
QY	385	GPKSSRNTLEAALNSIRYITRIHMKENDVREVVDWKFTAQVLDRIFLMLFLVVSVISGL	444

```
Db 381 GERVIAFLEKAADSIYRISRHVKDAFIQVQVQDKFVAQVLDRIFLMLFLVSVTGSV 440
Qy 445 GLFVPVVIYKWN 456
Db 441 LIFTPALQWLN 452

RESULT 7
I38056
nicotinic acetylcholine receptor beta-3 chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Aug-1999
C:Accession: I38056; S25587
R:Willoughby, J.J.; Ninkina, N.N.; Beech, M.M.; Latchman, D.S.; Wood, J.N.
Neurosci. Lett. 155, 136-139, 1993
A:Title: Molecular cloning of a human neuronal nicotinic acetylcholine receptor beta 3-1
A:Reference number: I38056; MUID:93390761; PMID:7690916
A:Accession: I38056
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-423 <RES>
A:Cross-references: EMBL:X67513; NID:934987; PIDN:CAA47851.1; PID:934988
C:Genetics:
A:Gene: GDB:CHRN3; ACHR
A:Cross-references: GDB:125222; OMIM:118508
A:Map position: 8p11.2-8p11.2
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 62.5%; Score 1534.5; DB 2; Length 423;
Best Local Similarity 68.6%; Pred. No. 1.6e-118;
Matches 286; Conservative 57; Mismatches 57; Indels 17; Gaps 3;
Qy 55 FQYERWRVPVEHLNDKIKIKFGIAISQVVDVEKQNLMTTNVWLKQEWIDVKLRWNPDD 114
Db 2 WKGYQKWRPVLHSNDTIKYFYGLKISQVVDVEKQNLMTTNVWLKQEWIDVKLRWNPDD 61
Qy 115 YGKIKVIRVPSDSVWTPDVLFDNADGRFEGT-STKTVIRYNGTVWTPPANYSKSTCID 173
Db 62 YGKIHKVPSESLWLPDVLFDNADGRFEGSLMTKVIKSNSTGVWTPPANYSKSTCID 121
Qy 174 VTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDVKDRDFDNGEWEIVSATGSKGNRTDS 233
Db 122 VTFPPFDQNCMKFGSWTYDGTWVDLILINENVDKDFDNGEWEILNAKMGKGNRRDG 181
Qy 234 CCWYPVTVTSFVTKRPLFLFTLIIIPICIGLSPLTVLFLVPSNEGEKICLCTSVLSLT 293
Db 182 VSYPTITYSFVLRLPLFTLIIIPICIGLSPLTVLFLVPSDEGEKLSLSTSVLSLT 241
Qy 294 VFLVIEELIPSSSKVPLTIGELVFTMIFVTLSIMVTFPAINIHRSSTHNAAPLVYR 353
Db 242 VFLVIEELIPSSSKVPLTIGELVFTMIFVTLSIIVTFVINVHRSSSTYHPMAPVWK 301
Qy 354 KIFLHPLKLLCMRSHVDYFT-QKEETES-----GSGPKSSRNTLEAAL 397
Db 302 RLFLQKLPLKLCMKDHDVRSSEKESQPVVKGVLEKKQKQSDGEKVLVAFLEKAA 361
Qy 398 NSRYITRHHMKNDREVVEDWKFIQVLDRLMPLFTLFPVSIIVSGSLGFLVPVIYKW 454
Db 362 DSIRYSIRHVKKEHFISQVQDKFVAQVLDRIFLMLFLVSVTGSVLIPTALKW 418

RESULT 8
A33523
nicotinic acetylcholine receptor beta-3 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jul-2000
C:Accession: A33523
R:Deneris, E.S.; Boulter, J.; Swanson, L.W.; Patrick, J.; Heinemann, S.
J. Biol. Chem. 264, 6268-6272, 1989
A:Title: Beta-3: a new member of nicotinic acetylcholine receptor gene family is expressed
A:Reference number: A33523; MUID:89197926; PMID:2703489
```

```
A:Accession: A33523
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-464 <DEN>
A:Cross-references: GB:J04636; NID:93298521; PIDN:AAC28887.1; PID:g205614
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 62.5%; Score 1534; DB 2; Length 464;
Best Local Similarity 65.1%; Pred. No. 1.9e-118;
Matches 286; Conservative 71; Mismatches 62; Indels 20; Gaps 3;
Qy 33 AQRLSEPSIIAKHEDSLKDLFQDYERWVRPVEHLNDKIKIKFGIAISQVVDVEKQNL 92
Db 24 ATAGL---SSVAEHEDALLRHLFGQYQKWRPVLNSSDIKVVYGLKISQVVDVEKQNL 80
Qy 93 MTNVLWKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLFDNADGRFEGT-STKTV 151
Db 81 MTNVLWKQEWIDVKLRWNPDEYGGINSIKVPSESLWLPDVLFDNADGRFEGSLMTKAI 140
Qy 152 IRYNGTVWTPPANYSKSTCIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDVKRD 211
Db 141 VKSGTGVSWTPPANYSKSTCIDVTFPPFDQNCMKFGSWTYDGTWVDLILINENVDKRD 200
Qy 212 FFDNGEWEIVSATGSKGNRTDSCWYPYVTVYFVIRKRLPLFTLIIIPICIGLSFLTVL 271
Db 201 FFDNGEWEILNAKMGKGNRRGFSYFPVTVYFVIRKRLPLFTLIIIPICIGLSFLTVL 260
Qy 272 FYLPNEGEKICLCTSVLSLTVFLVIEELIPSSSKVPLTIGELVFTMIFVTLSIMVT 331
Db 261 FYLPSEGEKLSLSTSVLSLTVFLVIEELIPSSSKVPLTIGELVFTMIFVTLSIIVT 320
Qy 332 VFAINIHRSSTHNAAPLVKRLFLHPLKLLCMRSHVDY-----FT 375
Db 321 VFVINHRSSTYHPMAPVWRKFLQRLPWLCKDPMDRFSFPDGKESDTRVGRKVS 380
Qy 376 QKEETESGSGPKSSRNTLEAALNSIRYITRHHMKNDREVVEDWKFIQVLDRLMFLWTF 435
Db 381 KRKQTPASDGERVLVAFLEKASESIRYISRHVKKEHFISQVQDKFVAQVLDRIFLWLF 440
Qy 436 LFVSIIVSGSLGFLVPVIYKW 454
Db 441 LIASVLGSLIIFIPALKW 459

RESULT 9
S16333
nicotinic acetylcholine receptor non-alpha-3 chain precursor - goldfish
C:Species: Carassius auratus (goldfish)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S16333
R:Caulley, K.; Agranoff, B.W.; Goldman, D.
J. Neurosci. 10, 670-683, 1990
A:Title: Multiple nicotinic acetylcholine receptor genes are expressed in goldfish retina
A:Reference number: S16333; MUID:90155434; PMID:2303867
A:Accession: S16333
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <CAU>
A:Cross-references: EMBL:M29529; NID:g212955; PIDN:AAA49167.1; PID:g212956
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 62.3%; Score 1531; DB 2; Length 466;
Best Local Similarity 64.8%; Pred. No. 3.4e-118;
Matches 283; Conservative 63; Mismatches 67; Indels 24; Gaps 3;
Qy 42 STAKHEDSLKDLFQDYERWVRPVEHLNDKIKIKFGIAISQVVDVEKQNLMTTNVWLKQ 101
Db 27 STAEWEDTLRLNLFRCYQKWRPVLNANDTITVRFGLKISQVVDVEKQHLMTTNVWLQ 86
Qy 102 EWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLFDNADGRFEGT-STKTVIRYNGTVW 160
```


[illegible]

Db 476 EAVEGGVCRSRSIQYCVPRDDAAPEADGQAAGALASRNTHTSABELPPDPQSPCKCTCKK 533

Qy 393 -----LEAALNSIRYIIRHIMKENDVREVVEDWKFTA 424

Db 536 EPSVSPSATVTKRSTKAPPHLPSPALTRAVEGVQYIADHLKAEDTDFSVKEDWKYVA 595

Qy 425 QVLDRMPLWTFLFVSI VGSGLFVP 449

Db 596 MVIDRIELMMFIIVCLLGTVGLFLP 620

RESULT 13

A26456

Nicotinic acetylcholine receptor alpha-4 chain, brain precursor - rat (fragment N; Alternate names: nicotinic acetylcholine receptor acetylcholine-binding chain C; Species: Rattus norvegicus (Norway rat) C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 13-Nov-1998 C; Accession: A26456; S02415

R; Goldman, D.; Deneris, E.; Luyten, W.; Kocher, A.; Patrick, J.; Heinemann, S. Cell 48, 965-973, 1987

A; Title: Members of a nicotinic acetylcholine receptor gene family are expressed A; Reference number: A26456; MUID: 87159533; PMID: 3829125

A; Accession: A26456

A; Molecule type: mRNA

A; Residues: 1-625 <GOL>

A; Cross-references: EMBL: M15681; NID: g205637; PID: g205638

R; Whiting, P.; Esch, F.; Shimasaki, S.; Lindstrom, J. FEBS Lett. 219, 459-463, 1987

A; Title: Neuronal nicotinic acetylcholine receptor beta-subunit is coded for by A; Reference number: S02415; MUID: 87276533; PMID: 3609304

A; Accession: S02415

A; Molecule type: protein

A; Residues: 'X', 28-30, 'X', 32, 'X', 34-36, 'X', 38-40, 'X', 42-43 <WHI>

C; Superfamily: acetylcholine receptor

C; Keywords: alternative splicing; glycoprotein; ion channel; neurotransmitter F; 1-26/Domain: signal sequence (fragment) #status predicted <SIG>

F; 27-625/Product: nicotinic acetylcholine receptor alpha-4 chain #status expected

Query Match 46.6%; Score 1145; DB 2; Length 625;

Best Local Similarity 39.08; Pred. No. 3.2e-86;

Matches 245; Conservative 83; Mismatches 108; Indels 192; Gaps 9

Qy 5 GSGPRALRLLLLVQVAGRCGLAGAGGAQGLSEPSIAKHESLLKDLFDYERWRVP 64

Db 1 GTCAPPPLLLPLLLLG-TGLLPAS-----SHIETRAHAEERLLKRLFSGYNKWSRP 52

Qy 65 VEHLNDIKTKIFGLAISQLDVVDKSNQLMNTNVLKQEMIDVKLRWNPDDYCGIKVIRVP 124

Db 53 VGNISDVLVPLFGLSIAQLIDVDSEKNQMTNVNWKQEWHDYKURWDPGDEVNVTISRIP 112

Qy 125 SDSVWTPDILVLFONADGRFEGTS-TKTVIRYNGTVTWTPTTPANYKSSCTIDVTFFFPDQON 183

Db 113 SELIWRPDIIVLYNADGDFAVTHLTKAHLFDGRVQWTPPAIKSSCSIDVTFFFPDQON 172

Qy 184 CSMKFGSWTYDGSQVDIILEDQDDVKRDFPDNGEWEIVSATSGSKGNRTDSCC--WYPYVT 241

Db 173 CTMKFGSWTYDKAKIDLVSIHSRVDQLDFWBSGEWIVDAVGTVYNTRYECCAEIYDPIT 232

Qy 242 YSFVikelPLPYTLFIIPICIGLSFLTVLVPYLSNEDGEKICLTSVLVSLTVFLLVIEE 301

Db 233 YAFIIRLPLFYTLNLIIPCLLISCLTVLVPYLPSECGEKVTLCLISVLVSLTVFLLLITE 292

Qy 302 IIPSSKVIPLIGELYVFTMI FVTLTSMVTVFALNIHRSSTSTNMAPLVKRKIFLHTLP 361

Db 293 IIPSTSLVPLIGELYLFTMI FVTLTSMVTVFALNVHRSRPTH-TMPANWRVRFIDIVP 351

Qy 362 KLLCMR-----SHVDYF----- 374

Db 352 RLLFMKRPVVYKDCNCRLLIESMHMKMANAPREWPEPBGILSDICNQLSPATFCNPT 411

Qy 375 ----- 374

Db 412 DTAVETQPTCRSPPLEVPDLKTSVEKASPCPSFGSCPPPKSSSGAPMLIKARSLSVQHV 471

Qy	377	-----KETESGSGPKSRNTLEA-----	-----ALNSRYVITHIM	408
Db	405	EGKGGCPCHPKEAIEDGCKVSRQTPQRAIVTTFVSVPSEIKQALSVKIIANMR	-----	464
Qy	409	KENDVREVVVDWKPIAQVLDRLMTLTFVSIVSGSLGFV	-----PVI	451
Db	465	SRNKAKEVDWDKYYAMVIDRIFLVFVFLVCVLGTLGLFLQPLI	-----	508

RESULT, 15
T09289,
nicotinic acetylcholine receptor alpha-6 chain precursor, neuronal - chicken
C;Species: Gallus gallus (Chicken)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: T09289
R;Gerzanich, V.; Kuryatov, A.; Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, February 1996
A;Description: Orphan alpha 6 AChR subunit forms a functional heteromeric receptor
A;Reference number: Z15638

Db 134 G-KTKALLRYDGMITWTTPPAIFKSSCPMDITFFPFHDHQCNSLKGFSWTYDKAKIDLLIIG 192

Ov 205 QDVDRKPFEDNGEWEIVSATSGSGKGNRTDSC--WYPVVTYSEVIKRLPLEVTLFLIIPCI 262

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193 SKVDNMNEFWSEWEI VDASGYRHDIIKYNCCBEIYTDITVSFYIRKLPMFYINLILPCL 252
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db

263 GLSFLTLVLFVLPSNEDGEKICLTCSVLVSIVTFLLVIEEIIIPSSKVIPLIGELYLVFTMI 322
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Qy

253 FLSFLTIVLFFVLPSDCGEKVTLCLISVLLSLTVFLLVITETIPTSTLSVIPLVGEYLLFTMI 312
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db

323 FYTLSIMVTVAINIHRSSSTHNAMAPLRVKIFLHTLPKLLCMRSHVDRYFTQ-KEETE 381
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Qy

313 FYTLSIVITVFVLIHYHRTPTTH-TMPRKWKTVFLSLLPKVLMQRPLEQBCKNI SKTK 371
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db

382 SOSGPGKSRRN-----T 392
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Qy

372 KGSAKTSCKSKXKHKKONKLHKQRCCHCDKADDLTSTRSRLSHQSLKXMAEHTEYSPE 431
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db

393 LEAALNSTRYTRHIKMENDVREVEDDKFIAOVLDRMFLWTFLFVSI VGSGLFLV-PVI 451
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:::
Qy

432 VKDVIDNNYQVFAENNKSGNETKEVEDDWKYVMVIDRVFLMWPII ILCVFGTAGLFIQPII 491
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Db

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Search completed: December 23, 2003, 21:24:21
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 21:23:42 ; Search time 345 Seconds
(without alignments)
253.342 Million cell updates/sec

Title: US-09-703-951A-8

Perfect score: 2456

Sequence: 1 NAARGSGPRALLLLVQLV.....PVIYKWNILPVHIGNANK 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2456	100.0	468	12	US-10-349-836-8
2	1586	64.6	458	12	US-10-349-836-16
3	1201.5	48.9	529	12	US-10-349-836-2
4	1169	47.6	528	10	US-09-892-985-2
5	1157.5	47.1	627	12	US-10-349-836-6
6	1135	45.2	494	12	US-10-349-836-10
7	1126.5	45.9	622	10	US-09-941-179A-3
8	1119	45.6	631	10	US-09-941-179A-7
9	1115	45.4	504	12	US-10-349-836-4
10	1102.5	44.9	502	15	US-10-157-031-92
11	1098.5	44.7	622	10	US-09-941-179A-11
12	1087	44.3	504	10	US-09-892-985-4
13	1082.5	44.1	627	10	US-09-892-985-6
14	1062.5	43.3	479	12	US-10-349-836-20
15	1028.5	41.9	498	12	US-10-349-836-18

Sequence 12, Appl
Sequence 28, Appl
Sequence 69, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 2, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 56, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 38, Appl
Sequence 144, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 8, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 86, Appl
Sequence 132, Appl

US-10-349-836-8
Sequence 8, Application US/10349836
Publication No. US20030138911A1
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
Harpoit, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

ALIGNMENTS

RESULT 1

US-10-349-836-8
Sequence 8, Application US/10349836
Publication No. US20030138911A1
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
Harpoit, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

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;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-349-836-8

Query Match 100.0%; Score 2456; DB 12; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.4e-233; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;

Qy 1 MAARGSPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYER 60
Db 1 MAARGSPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYER 60
Qy 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQMLTNTVWLKQEWIDVKLRWNPDDYGGIKV 120
Db 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQMLTNTVWLKQEWIDVKLRWNPDDYGGIKV 120
Qy 121 IRVPSDSVWTPDVLVFNADGRFGTSTKTVIRYNGVTWTPPANYKSSCTIDVTREPPD 180
Db 121 IRVPSDSVWTPDVLVFNADGRFGTSTKTVIRYNGVTWTPPANYKSSCTIDVTREPPD 180
Qy 181 LQNCMKFGSWTVDGSDVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYV 240
Db 181 LQNCMKFGSWTVDGSDVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYV 240
Qy 241 TYSFVIRKRLPFTFLIIPCIGLSFLTIVLVFVLPSEGEKICLCTSVLSVLTFLVIE 300
Db 241 TYSFVIRKRLPFTFLIIPCIGLSFLTIVLVFVLPSEGEKICLCTSVLSVLTFLVIE 300
Qy 301 EIIPSSSKVPLIGEYLVFTMIFTLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTL 360
Db 301 EIIPSSSKVPLIGEYLVFTMIFTLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTL 360
Qy 361 PKLLCMRSHVDVRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420
Db 361 PKLLCMRSHVDVRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420
Qy 421 KFTAQVLDRLMFLTFLFVSVIGSLGLFPVPIYKWNILIPVHIGNANK 468
Db 421 KFTAQVLDRLMFLTFLFVSVIGSLGLFPVPIYKWNILIPVHIGNANK 468

RESULT 2
US-10-349-836-16
; Sequence 16, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; ADDRESS: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-349-836-16

Query Match 64.6%; Score 1586; DB 12; Length 458;
Best Local Similarity 65.8%; Pred. No. 1.9e-147;
Matches 302; Conservative 63; Mismatches 66; Indels 28; Gaps 5;

Qy 13 LLLVLQVLAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKI 72
Db 6 MLVLVL-----GIPSSATGTF---NSIAENEDALLRHLFGQYKQWVRPVLHNSDTI 54
Qy 73 KIKFGLAISQLVDVDEKQMLTNTVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPD 132
Db 55 KYVFGGLKISQLVDVDEKQMLTNTVWLKQEWIDVKLRWNPDDYGGIHSIKVPSESLWLPD 114
Qy 133 IVLFDNADGRFECT-STKTVIRYNGVTWTPPANYKSSCTIDVTFFPFDLQNCMKFGSW 191
Db 115 IVLFDNADGRFEGSLTKVIVKNGVTWTPPASYKSSCTMDVTFFPFDQNCMKFGSW 174
Qy 192 TYDGSQVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYVTVYSFVIRKRLPL 251
Db 175 TYDGTWVDLILINENVDKDPFDNGEWEILNAGKMGNNRDGVVSPFTYTSFVLRRLPL 234
Qy 252 FYTLPLIIPCIGLSFLTIVLVFVLPSEGEKICLCTSVLSVLTFLVIEIIPSSSKVIP 311
Db 235 FYTLPLIIPCIGLSFLTIVLVFVLPSEGEKLSLSTSVLSVLTFLVIEIIPSSSKVIP 294
Qy 312 LIGELYLVFTMIFTLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTLKLKCMRSHVD 371
Db 295 LIGELYLVFTMIFTLSIIVTVFVINVHRRSSSTHPMAPWPKKFLQKLPKLCMKDHDV 354
Qy 372 RYFT-QKEETES-----GSGPKSSRNTLEAALNSIRYITRHKENDVRE 415
Db 355 RYSSPEKEESQPVVKGKVKLKKQKQLSDGKLVAFLEKAAADSIRYISRHVKEHFIQ 414
Qy 416 VVEDWKFIAQVLDRLMFLTFLFVSVIGSLGLFPVPIYKW 454
Db 415 VVQDWKFIAQVLDRLMFLTFLFVSVITGSLVLTFLPALKMW 453

RESULT 3
US-10-349-836-2
; Sequence 2, Application US/10349836
; Publication No. US20030138911A1
```

Query Match	47.6%;	Score 1169;	DB 10;	Length 528;
Best Local Similarity	49.9%;	Pred. NO. 3e-106;		
Matches 241; Conservative	65;	Mismatches 105;	Indels 72;	Gaps 9


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333 TTH-TMPRWKVTVELKLLOVQLMRWPLDKTRGTGSDAVPRGLARPAPKAQKLIASHGEPRH 391
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
373 ----YFTQKEETSGSGPKSRNTL-----EALNSIRIYITRHKENDVRE 415
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
392 LKECFCHCKSNELATSKRRLSHOPLQWVVENSHPESVEDVINSVOFIAENMKSHNETKE 451
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
416 VVEOWKFTAQVLDRMFLWTTLFFSVISVSLGLGFVPVIYKWANILIPVHIIGNANK 468
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
452 VEDWDKYVMVDVRVFWLFVIIICVFCTAGLFLOPL-----LGNTGK 493
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||

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US-09-941-179A-3
; Sequence 3, Application US/09941179A
; Patent No. US20020146765A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Acetylcholine receptor subunits
; FILE REFERENCE: Le A 34 821
; CURRENT APPLICATION NUMBER: US/09/941,179A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: DE 100 42 177.6
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
; OTHER INFORMATION: receptor
US-09-941-179A-3

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Best Local Similarity	38.9%;	Pred. No. 6e-102;		
Matches	229;	Conservative	78;	Mismatches 98; Indels 183; Gaps 7;
QY	44	AXHEDSLKOLFQDYERWRVPEVHLNDKIKFKGLAISQLVDVDEKNQIMTTNVMLKQSW	103	
Db	29	AHAERLLKCLFGYGNKWSRPVANISDVVLRFGLSIAQLIDVDEKNQIMTTNVVVKQSW	88	
QY	104	IDVKLRWNPDDYGGGIKVIKVPESDSVMTDVLFDNADGRFECT-STKTVIRNGTVTWTTP	162	
Db	89	HDYKLRWNPQEVNVTISRIPSELIRWPDIVLYNNADGNFVTLTKATLNTVGRVEMRP	148	
QY	163	PANYKSSCTIDVTFPPFDLQNCMKFSGWTYDGSQVDIILEDDQVDKDRFPDNGSWEIVS	222	
Db	149	PAIYKSSCEIDVEYFPFOQTCVMKFGSWTYDKAKIDLVSMHSHVDQLDYWSEGEWIIIN	208	
QY	223	ATGSKGNRTDSCW--YPVTVSYFVIKRPLFYTLFLIIPCIGLSFLTVLVFLYPLSNEGE	280	
Db	209	AVGNVNSKKYECCTEIIYDITVSFIIRLPLFYTLNLIIIPCLLISCLTVLVFLYPLSECE	268	
QY	281	KICLCTSVLVSLTVPELLVIEIIPSSKVIPLIGBYLVFTMIFVTLSIMTVFVAINIHR	340	
Db	269	KITLCISVLLSLTVPELLITEIIPSTSLVPLIGBYLLFTMIFVTLIIITVFLVNLVHR	328	
QY	341	SSSTHNANAPLVKRIFLHTLPKLLCMR-----SHVD-----	367	
Db	329	SPRTH-TMPDWVRRVFLDIPVRLPFMPKRPSTVKONCKKLISMHKLITNSPRLWSETDMEP	387	
QY	368	-----SHVD-----	371	
Db	388	NFTTSSSPSQSNEPSPTSSFCALHEEPAKPMCKSPSGQYSNLHPPEPQVTCSPKPSCH	447	
QY	372	-----RYFTQKEETSGS-----	384	
Db	448	PLSDTQTTSISKGRSLSVQQMYSPNKTEEGSIRCKRSIOICYLQEDSSQTNHGHSASGA	507	
QY	385	-----GPKSSRN-----	401	

Query Match	46.2%;	Score 1135;	DB 12;	Length 494;
Best Local Similarity	46.1%;	Pred. No. 6.2e-103;		
Matches 218;	Conservative 89;	Mismatches 102;	Indels 64;	Gaps 7;
QY	47	ESLLKDLFDQYERWRVPVHLNDKIKIKGLAISQLVDYDERKNQLMTTNVLKQEWIDV	106	
Db.	34	EERLFHKLFSHYNQFIRPVENVSDPVTVHFEVAITQLANDEVNQIMETNLWLRIHWNDY	93	
QY	107	KLRWNPDDYGGIKIVIRPSPSVMTDPDVLFDNADGRF--EGTSTKTVIRYNGVTWTPPA	164	
Db	94	KLRWDPMEDYIGIETLRVPADKIKWPKDPVLVYNNAVGDFQVEG-KTKALLKNGIMTWTTPA	152	
QY	165	NYKSSCTIDVTPFPFDLQNCMKFGSWTYDGSQVDIILEDQDDKDRDFPONGWEIVSAT	224	
Db	153	IFAKSSCPMDITFPFPFHQNCSLAFGSWTYDKABIDILLIIGSKVDMNDFWENSWEIIDAS	212	
QY	225	GSKGNRTDSCC--WYPVVTYSFYKRLPLPYTLFLIIPCIGLGLTVLVYFLSPNEGEKI	282	
Db	213	GKYGHDIKYNCCBIEYTDITYSFYIRRLPMYETNLIIPCLFISGLTVLVYFLSPDCGEKV	272	
QY	283	CLCTSVLVSLTVELLVIEEIPSSKVIPLIGBYVFTMI FVTLISIMVTVFAINIHRSS	342	
Db	273	TLCISVLVSLTVELLVITETIPSTSLVWPLVGEYLLFTMIFVTLISIVTVFVLNIHVRTP	332	
QY	343	STHNAMAPIVRKTI FLHTLPKLLCMWRSHVDV-----	372	

Db 508 SORCHLNBEQPHKPHQCKCRKGEAAAGTPTQGSKSHNKGHEHVLVLMSPALKLAVEGVH 566
 Qy 402 YITRHIMKENDVREVEDWKFIQAQVLDRLMFLMTWTLFVSVIGSLGLFVP 449
 Db 568 YIADHLRAEDADFVKEDMKYVAMVIDRFLWMFIIVCLLGTGVGLF 615
 RESULT 8
 US-09-941-179A-7
 ; Sequence 7, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 631
 ; TYPE: ERT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-7
 Query Match 45.6%; Score 1119; DB 10; Length 631;
 Best Local Similarity 38.5%; Pred. No. 3.3e-101;
 Matches 230; Conservative 81; Mismatches 94; Indels 192; Gaps 8
 Qy 44 AKHDSLLKDLFDQYERWVRPVEHUNDKIKIKFGLAISQVLDVDEKQMLTNNVWLKQEW 103
 Db 29 AHAERLLKKLFSGYKNKSRPVANISDVLRVFGLSIAQLIDVDEKQMMTTNVVWKQEW 88
 Qy 104 IDVKLRWNPDDYGGIKVIRKPSDSVWTPDIVLFDNADGRFEGTS-TKTIVIRNGVTWTP 162
 Db 89 HDYKLRNDPQBYENWTSIRIFSELIRRPDIVLNNADGDFAVHTUKAHLFYDGRKKNWP 148
 Qy 163 PANYKSSCTIDVTFFPPDLQCNMKFGSWTYDGSQVDII-----LEDQDVDRKDF 213
 Db 149 PAIYKSSCSIDVTFFPPDQCNMKFGSWTYDKAKIDLVSMSHRGTNVVELGVLDQLDVW 208
 Qy 214 DNGWEIVSATSGKGNRTDSCW--YPVTVYSFVTKRLPLFVTLFLIIPICGLSFLTVLV 271
 Db 209 ESGEWVIAINAVGNTYNSKKYECCTEIPYDITYSFIIIRRLPLFYITNLIIPCLLISCLTVLV 268
 Qy 272 FYLPSNGEKICLCSTVLVSLTVFLLVTEIIIPSSSKVPLPIGELYVFTMIPTVLSIMVT 331
 Db 269 FYLPSECEGKITCLCSVLVSLTVFVLLLTETIIPSTSLVPLIGELYLFTMIPTVLSIIIT 328
 Qy 332 VFALNIHRSSSTHNAMAPLVKRIPLHTLPKLLCMR-----SHVD----- 371
 Db 329 VFVLNVHRSRPTH-TMEDWVRVFLDIVPRLLFMKRPSTVKDNCKKLIESMHKLTNSRP 387
 Qy 368 -----SHVD----- 371
 Db 388 LWSETMEPNFTSSSPSQSNERSPTSSFAHLEERAPKCMCKSPGQVYMLHPPPPQVT 447
 Qy 372 -----RYFTQKEETESGS----- 384
 Db 448 CSSPKPSCPILSDTQTTSISKRSLSVQOMYSFNKTEBGSIRCRSRSTQYCYVLQEDSSQT 507
 Qy 385 -----GPKSSRN-----T 392
 Db 508 NGHSSASPASORCHLNBEQPHKPHQCKCRKGEAAAGTPTQGSKSHNKGHEHVLVLMSPA 567
 Qy 393 LEAALNSIRYTRIMKENDVREVEDWKFIQAQVLDRLMFLMTWTLFVSVIGSLGLFVP 449

Db 165 PFFDYQNTMGWSYDKAKIDLVLISSWNLKDYWESGEWAIKAPGYKHDIKYNCE 224
Qy 236 -WYPVYTSFVVKRLPLFYTLFIIPICIGLSFLTVLFLYPSNEGEKICLCTSVLVSJTV 294
Db 225 EYIPDITYSLVIRRLPLFYTLFIIPICLLISFLTVLFLYPSDCGEKVTLCISVLSJTV 284
Qy 295 FLLVIEEIPSSKVIPIGLIYVFTMIPLVFTLIMVTVPAINIHRSSSTTNAMAPLVRK 354
Db 285 FLLVITIPSTSLVPIGLIYVFTLIMVTVPAINIHRSSSTTNAMAPLVRK 354
Qy 355 IFLHLPKLLQMR----- 367
Db 344 VFLNLLPRVMTPTSGNEGNAQPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGY 403
Qy 368 -----SHVDYFTQKEETESGPKS-----SRNTLEAALNSIRYITRHKMKENDVREV 416
Db 404 CHRRRIKISFNANLTSRSSSESVDVLSGALSPEIKATQSVKYIAENKMAQNEAKEI 463
Qy 417 VEDWKFAIQVLDRLMFLWTFVLSVIGSLGFV 448
Db 464 QDDWKYVAMVIDRIFLWVFTLVLCILGTAGLEL 495

RESULT 10
US-10-157-031-92
; Sequence 92, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; CURRENT APPLICATION NUMBER: US/10157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 92
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-92

Query Match 44.9%; Score 1102.5; DB 15; Length 502;
Best Local Similarity 43.2%; Pred. No. 1e-99;
Matches 220; Conservative 93; Mismatches 119; Indels 77; Gaps 6;
Qy 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAQGLSEPSIAKHEDSLKDLFQDYER 60
Db 1 MALAVSLPLACRALLLLLS-----LLPVARASEAHRFLERLFEDYNE 45
Qy 61 WRPVEHLNDKIKIFGLAISQVVDVEKQMLTNNVWLKQEWIDVLRWNPDDYGGIKV 120
Db 46 IIREVANVSDPVIIHFEVMSQLVKVDENVQIMETNLWKQIWDYKLNWPNPSSGGYGAEF 105
Qy 121 IRVPSDSVWTPDVLVFNADGRF-GTSTKTVIRYNGTVTTPPANKSSCTIDVTPFP 179
Db 106 MRVPAQKIKRPDVLVYNNAVGDVQTKTKALLKYTGVTWIPAIKSSCKIDVTPFP 165
Qy 180 DLQCSMKFGSWTYDGSQVDIILEDQVDKDFDNGEWEIVSATGSGNRTDSC--WY 237
Db 166 DYQNTWKFGWSYDKAKIDLVLISSWNLKDYWESGEWAIKAPGYKHDIKYNCEIY 225
Qy 238 PYVYTSFVVKRLPLFYTLFIIPICIGLSFLTVLFLYPSNEGEKICLCTSVLVSJTV 297
Db 226 PDITYSLYRRLPLFYTLFIIPICLLISFLTVLFLYPSDCGEKVTLCISVLSJTV 285
Qy 298 VIEEIPSSKVIPIGLIYVFTMIPLVFTLIMVTVPAINIHRSSSTTNAMAPLVRK 357
Db 286 VITETIPSTSLVPIGLIYVFTLIMVTVPAINIHRSSSTTNAMAPLVRK 357

Qy 358 HTLPKLLQMR----- 367
Db 345 NLLPRVMTPTSGNEGNAQPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGYCHH 404
Qy 368 -----SHVDYFTQKEETESGPKS-----SRNTLEAALNSIRYITRHKMKENDVREV 419
Db 405 RRIKISFNANLTSRSSSESVDVLSGALSPEIKATQSVKYIAENKMAQNEAKEI 464
Qy 420 WKFAIQVLDRLMFLWTFVLSVIGSLGFV 448
Db 465 WKYVAMVIDRIFLWVFTLVLCILGTAGLEL 493

RESULT 11
US-09-941-179A-11
; Sequence 11, Application US/09941179A
; Patent No. US20020146765A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Acetylcholine receptor subunits
; FILE REFERENCE: Le A 34 821
; CURRENT APPLICATION NUMBER: US/09/941.179A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: DE 100 42 177.6
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
; OTHER INFORMATION: receptor
US-09-941-179A-11

Query Match 44.7%; Score 1098.5; DB 10; Length 622;
Best Local Similarity 38.3%; Pred. No. 3.4e-99;
Matches 225; Conservative 79; Mismatches 101; Indels 183; Gaps 7;
Qy 44 AKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQVVDVEKQMLTNNVWLKQEW 103
Db 29 AHAEERLLKKLFSGYNKWSRPVANISDVLRVFLGSLAQIDVDEKQNMNTNVWKQEW 88
Qy 104 IDVKLRNPDYGGIKVIRVPSDSVWTPDVLVFNADGRFGTS-TKTVIRYNGTVTTP 162
Db 89 HDYKLRWDPOEYENVTVSIRIPSELIRPDIVLVYNADGDFAVTHLTKAHLFYDGRKWWP 148
Qy 163 PANKSSCTIDVTPFPDLQCSMKFGSWTYDGSQVDIILEDQVDKDFDNGEWEIVS 222
Db 149 PAIYKSSCSIDVTPFPDQCNKMGKFGSWTYDRAKIDLVSMHSHVDLSEFVTSVEWDLLE 208
Qy 223 ATGSGNRTDSCCWYPY--VTYGFVIRKRLPLFYTLFIIPICIGLSFLTVLFLYPSNEGE 280
Db 209 VPAVRNEKFTCCDEPYLDITENFIIRRLPLFYTLFIIPICLLISCLTVLFLYPSSECE 268
Qy 281 KICLCTSVLVSJTVLFLYPSNEGEKICLCTSVLVSJTVLFLYPSNEGE 340
Db 269 KITICISVLSJTVLFLYPSNEGEKICLCTSVLVSJTVLFLYPSNEGE 328
Qy 341 SSSTHNAAPLVRKIFLHLPKLLQMR----- 367
Db 329 SPRTH-TMPDVRVRFVDIVPRLLFMKRPSTVKDNCKKLESMMKLTNSPRLNSETDMEP 387
Qy 368 -----SHVD----- 371
Db 388 NFTTSSSPSQSNEPSTSSFCALHEBPAPKPMCKSPSGQYSLMHPPEPQVTCSSPKPSCH 447
Qy 372 -----RYFTQKEETESG----- 384
Db 448 PLSDTQTTISIKGRSLSVQOQMYSPNKTEGSIKRSRSIQCYLQEDSSQTNHSSASPA 507

QY 385 -----GPKSSRN-----TLEAALNSIR 401
DB 508 SQCHLINEPOQHPQCKCKRGEAGTPTGSGSKSHNGEHLVLMSPALKLAVEGVH 567
QY 402 YITRHKENDREVEDMKFIAQVLDRLMFLWTLFVSVISGLFLVP 449
DB 568 YIADHLRAEDADFSVKEDWKYVAMVIDRIFLWMFIIVCLLGTGVLFLP 615

RESULT 12
US-09-892-985-4
; Sequence 4, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-985-4

Query Match 44.3%; Score 1087; DB 10; Length 504;
Best Local Similarity 42.4%; Pred. No. 3.4e-98;
Matches 217; Conservative 94; Mismatches 115; Indels 86; Gaps 8;
QY 5 GSGPRAL-----RLLLVQLVAGRCGLAGAGGAGLSEPSSTAKHEDSLKQLPQD 57
DB 2 GSGFLSLPLALSPRLLLL-----LSLTPVARASEAHRFLERLFD 44
QY 58 YERWAPVEHLNDKIKFKGLAISQLVDVDEKQLMTTNVWLKQEWIDVLRWNPDDYGG 117

DB 45 YNEIIRPVANSDPVIHFESMSQLVKVDEVNQIMETNLWLKQIWXDYKLKNPSPDYG 104
QY 118 IKVIRVPSDSVMTDVLFDNADGRFE-GTSTKTVIRYNGTWTWTPPANYKSSCTIDVTF 176
DB 105 AEFMRVPAQKIWKPDVLVNNVAVGDFQDDKTKALKKYTGVTWIPPAIFKSSCKIDVTY 164
QY 177 FFPDLQNCMKFGSWTYDGSQVDIILEDQDVDRKDFDNGEWEIFVATSGKGNRTDSCC- 235
DB 165 FFPDYQNCMTKFGWSYDKAKIDLVLGSSMNLKDYWESGEWAIKAPGVNHDIKYNCC 224
QY 236 -WYPVYTVSFVIRKRLPLFYTLFLIIPICIGLSFLTVLVFLPSNEGKICLCTSVLSLTV 294
DB 225 EIVPDITYSLIIRRLSLFYTLIIPWLIISFTIVVVFVLPSCGCKVTLICISVLSLTV 284
QY 295 FLIVIEEIIIPSSSKVPLIGELVFTMIFVTLISIMVTVPAINTHRSSSTHNAAPLVK 354
DB 285 FLIVITETIPSTSLVPLIGELVFTMIFVTLISIMVTVPAINTHRSSSTHNAAPLVK 343
QY 355 IFLLHTLPKLLCMRSHVD-----RYTQKEETESGSG----- 385
DB 344 VFLNLLPRVMEWTRPTSNENNAQKPRPLYCAELSNLNCFSRAESXGCKEGYPCQDGMCGY 403
QY 386 -----PKSSRNTLEA-----ALNSIRVITRHKENDVREV 416
DB 404 CHHRIKISNFSANLTRSSSESVDVLSLSALSPEIKAEIQSVKYIAENMKQAQNEAKEI 463
QY 417 VEDWKEIAQVLDRLMFLWTLFVSVISGLFLV 448
DB 464 QDDWKYVAMVIDRIFLWVTLVCTLTGTLGL 495

RESULT 13
US-09-892-985-6
; Sequence 6, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360

```

CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-349-836-20

Query Match 43.3%; Score 1062.5; DB 12; Length 479;
Best Local Similarity 44.2%; Pred. No. 8.3e-96;
Matches 209; Conservative 86; Mismatches 99; Indels 79; Gaps 8;

QY 47 EDSLKDLFQDYERWRVVEHLNDKIKIEGLAISQLVDDYDEKNQLMTTNVLKQEWIDV 106
DB 34 EERLFHKLFSHYNQFIRFVENVSDDPTVVFHEVAITQLANV-----IWN DY 78

QY 107 KLRWNPDDYGGIKVIRVPDSVWTPDIVLFDNADGRF--EGTSTKTVIRYNGTWTTPPA 164
DB 79 KLRWDPMEYDGIETLRAVPADKIWKPDIVLYNNAVGDFQVEG-KTKALLKXNGMITWTPPA 137

QY 165 NTKSSCTIDVTFFPFDLQNCMKFGSWTYGSGOVDIILEDQVDKRDFFDNGSEIVSAT 224
DB 138 IFKSSCPMDITFFPFDHQNCSLKFGSWTYDKAEIDLLIIGSKVDMDNDFWENSEWEIIDAS 197

QY 225 GSKGNRTDSCC--WYPYVTVSYFKELPLPYTLFLIIPCLIGLSFLTFLVFLYLSNEGEKI 282
DB 198 GYKHDIKYNCCEBEIYTDITYSYFIRLPMFYTNLIIPCLIFSLTFLVFLYLPDCEKV 257

QY 283 CLCTSVLSLTFLVLLVIEBIIIPSSSKVILPGLBYLFTMTIFVTLTIMVTFAINIHRSS 342
DB 258 TLCTSVLSLTFLVLLVITETIPSTSLVPLVGEYLLFTMTIFVTLTIMVTFVNIHYRTP 317

QY 343 STHNAMAPLVRKIFLHTLPLKLLCMRSHVD----- 372
DB 318 TTH-TMPRWKTVFLKLLPQVLLMRWPLDKTRGTGSDAVPRGLARRPAKGLASHGEPRH 376

QY 373 ----YFTQKEETESGCPKSSRNTL-----EALNLSIRYITRTHINKENDVRE 415
DB 377 LKECFCHCHSNELATSKRSLSHQPLQWVYVENSEHSESPEDVINSVQFIAENKMSHNETKE 436

QY 416 VVEDWKEFIAOVLDRMFMTFLFVSIYVSGLSGLFVPVTVYKWNATILIPVHIGNANK 468

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[illegible][illegible]

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OM protein - protein search, using sw model

Run on: December 23, 2003, 21:19:52 ; Search time 29 Seconds
(without alignments)
682.810 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKWNILIPVHGNANK 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pdp:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pdp:*
5: /cgn2_6/ptodata/2/iaa/PTJUS_COMB.pdp:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2456	100.0	468	US-08-487-596-8	Sequence 8, Appli
2	2456	100.0	468	US-08-660-451A-8	Sequence 8, Appli
3	1586	64.6	458	US-08-660-451A-16	Sequence 16, Appl
4	1582	64.4	458	US-08-487-596-16	Sequence 16, Appl
5	1582	64.4	458	US-08-484-722-4	Sequence 4, Appli
6	1201.5	48.9	529	US-08-496-855A-2	Sequence 2, Appli
7	1201.5	48.9	529	US-08-487-596-2	Sequence 2, Appli
8	1201.5	48.9	529	US-08-660-451A-2	Sequence 2, Appli
9	1179	48.0	511	US-08-464-258B-4	Sequence 4, Appli
10	1169	47.6	528	US-08-466-589-2	Sequence 2, Appli
11	1169	47.6	528	US-08-700-636-2	Sequence 2, Appli
12	1169	47.6	528	US-08-467-574-2	Sequence 2, Appli
13	1169	47.6	528	US-09-217-345-2	Sequence 2, Appli
14	1168.5	47.6	510	US-08-278-635B-4	Sequence 4, Appli
15	1168.5	47.6	510	US-08-471-961-4	Sequence 4, Appli
16	1157.5	47.1	627	US-08-660-451A-6	Sequence 6, Appli
17	1137	46.3	629	US-08-464-258B-6	Sequence 6, Appli
18	1135	46.2	494	US-08-487-596-10	Sequence 10, Appl
19	1135	46.2	494	US-08-484-722-2	Sequence 2, Appli
20	1135	46.2	494	US-08-660-451A-10	Sequence 10, Appl
21	1132	46.1	629	US-08-278-635B-6	Sequence 6, Appli
22	1132	46.1	629	US-08-471-961-6	Sequence 6, Appli
23	1132	46.1	629	US-08-660-451A-4	Sequence 4, Appli
24	1108.5	45.4	504	US-08-660-451A-4	Sequence 4, Appli
25	1093.5	44.5	497	US-08-487-596-6	Sequence 6, Appli
26	1093.5	44.5	497	US-08-278-635B-5	Sequence 5, Appli
27	1093.5	44.5	497	US-08-464-258B-5	Sequence 5, Appli
28	1087	44.3	504	US-08-466-589-4	Sequence 4, Appli
29	1087	44.3	504	US-08-700-636-4	Sequence 4, Appli
30	1087	44.3	504	US-08-467-574-4	Sequence 4, Appli
31	1087	44.3	504	US-09-217-345-4	Sequence 4, Appli
32	1082.5	44.1	627	US-08-466-589-6	Sequence 6, Appli
33	1082.5	44.1	627	US-08-700-636-6	Sequence 6, Appli
34	1082.5	44.1	627	US-08-467-574-6	Sequence 6, Appli
35	1082.5	44.1	627	US-09-217-345-6	Sequence 6, Appli
36	1062.5	43.3	479	US-08-660-451A-20	Sequence 20, Appli
37	1050	42.8	504	US-08-487-596-4	Sequence 4, Appli
38	1028.5	41.9	498	US-08-487-596-18	Sequence 18, Appl
39	1028.5	41.9	498	US-08-660-451A-18	Sequence 18, Appl
40	1016.5	41.4	457	US-08-278-635B-3	Sequence 3, Appli
41	1016.5	41.4	457	US-08-471-961-3	Sequence 3, Appli
42	1016	41.4	458	US-08-464-258B-3	Sequence 3, Appli
43	1015.5	41.3	498	US-08-496-855A-6	Sequence 6, Appli
44	1015.5	41.3	498	US-08-466-589-12	Sequence 12, Appl
45	1015.5	41.3	498	US-08-700-636-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-08-487-596-8
; Sequence 8, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-596-8

Query Match      100.0%; Score 2456; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAGQRLSEPPSSIAKHEDSLKDLFDQYER 60
Db 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAGQRLSEPPSSIAKHEDSLKDLFDQYER 60
Qy 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTNNWLKQEWIDVKLRWNPDDYGGIKV 120
Db 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTNNWLKQEWIDVKLRWNPDDYGGIKV 120
Qy 121 IRVPSDSVWTPDVLFDNADGRFEGTSTKTVIRYNGTWTTPPNYKSSCTIDVTFPPFD 180
Db 121 IRVPSDSVWTPDVLFDNADGRFEGTSTKTVIRYNGTWTTPPNYKSSCTIDVTFPPFD 180
Qy 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKRDFFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
Db 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKRDFFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
Qy 241 TYSFVIRKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLSVTLVFLLVIE 300
Db 241 TYSFVIRKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLSVTLVFLLVIE 300
Qy 301 EIIPSSSKVPLIGEYLVFTMI FVTLISIMVTVPAINIHRRSSSTHNAMAPLVKIFLHTL 360
Db 301 EIIPSSSKVPLIGEYLVFTMI FVTLISIMVTVPAINIHRRSSSTHNAMAPLVKIFLHTL 360
Qy 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
Db 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
Qy 421 KFTAQVLDRLMFLTWTFVSVIGSLGFLVPVIYKWNILIPVHIGNANK 468
Db 421 KFTAQVLDRLMFLTWTFVSVIGSLGFLVPVIYKWNILIPVHIGNANK 468

RESULT 2
US-08-660-451A-8
; Sequence 8, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-596-8

Query Match      100.0%; Score 2456; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAGQRLSEPPSSIAKHEDSLKDLFDQYER 60
Db 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAGQRLSEPPSSIAKHEDSLKDLFDQYER 60
Qy 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTNNWLKQEWIDVKLRWNPDDYGGIKV 120
Db 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTNNWLKQEWIDVKLRWNPDDYGGIKV 120
Qy 121 IRVPSDSVWTPDVLFDNADGRFEGTSTKTVIRYNGTWTTPPNYKSSCTIDVTFPPFD 180
Db 121 IRVPSDSVWTPDVLFDNADGRFEGTSTKTVIRYNGTWTTPPNYKSSCTIDVTFPPFD 180
Qy 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKRDFFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
Db 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKRDFFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
Qy 241 TYSFVIRKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLSVTLVFLLVIE 300
Db 241 TYSFVIRKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLSVTLVFLLVIE 300
Qy 301 EIIPSSSKVPLIGEYLVFTMI FVTLISIMVTVPAINIHRRSSSTHNAMAPLVKIFLHTL 360
Db 301 EIIPSSSKVPLIGEYLVFTMI FVTLISIMVTVPAINIHRRSSSTHNAMAPLVKIFLHTL 360
Qy 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
Db 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
Qy 421 KFTAQVLDRLMFLTWTFVSVIGSLGFLVPVIYKWNILIPVHIGNANK 468
Db 421 KFTAQVLDRLMFLTWTFVSVIGSLGFLVPVIYKWNILIPVHIGNANK 468

RESULT 3
US-08-660-451A-16
; Sequence 16, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
```

RESULT 4
US-08-487-596-16
US-08-487-596-16, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Elliot, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:

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08-07-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-596-16

Query Match      64.4%; Score 1582; DB 4; Length 458;
Best Local Similarity 65.8%; Pred.No. 7.3e-161;
Matches 302; Conservative 62; Mismatches 67; Indels 28; Gaps 5;

QY   ... 13...LLLVVAGRCGLAGAAGGAGRLSEPPSSIAKHEDSLKDLFDYERWVRPV...EHLDKI 72
DB   ... 6 MLVLIVL-----GI PSSATTFG---NSIAENEDALLRHFLFGYQKWVRPVLHSDTI 54

73 KIKFGLAISOLVDVDEKNQLMTTNVWLKQSWIDVKLRWNPDYGGIKVIRVPDSVWTPD 132
DB   55 KYVFGLKISOLVDVDEKNQLMTTNVWLKQSWTHDKLRWNPDYGGIHSIKVPSESLLWLPD 114

133 IVLFDNADGRFECT-STKTIVIRYNGVTVTTPPNKYSSCTCIDVTFFPFDFLQNCSMKFGSW 191
DB   115 IVLFEFNADGRFEGSLMTKVTKSNGTVMTPPPASYSKSCCTMDVTFFPFDFRONCSMKFGSW 174

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Query Match 64.4%; Score 1582; DB 4; Length 458;
Best Local Similarity 65.8%; Pred. No. 7.3e-161;

Best Local Similarity	65.6%;	Pied: NO. 7.3e-161;
Matches 302;	Conservative	62; Mismatches 67;
Indels	28;	Gaps 5;

Y. 13 L L L L V Q V A G R C G L A A G G A Q R G L S E P S I A K H E D S L L K O L F Q D Y E R W V R P V E H L N D K I 72

73 KIKEGI,ATSUO,YDVDEKNOI,MTTNVWL,KOEWT,DVKI,BWNPDDYGGIKVIRVPSDSVWTPD 132

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[illegible]

115 I V L F E N A D G R F E G S L M T K V I V K S N G T V V W T P P A S Y K S S C T M D V T F F F P D R Q N C S M K F G S W 174

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QY      192 TYDGSQVDIILDDQVDRKDFPDNGEWSIVSATGSKGNRTDSCWYPVTYSFVIKRLEL 251
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      175 TYDGTWVDLILINENVDRKDPFDNGEWEIFLNAGMKGNRRDGVVSPFITYSFVLRLPL 234

QY      252 FYTLFLITPCIGLSFLTVLVLYPSNEGEKICTSVLSITVFLLVIEEIIIPSSSKVIP 311
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      235 FYTLFLITPCIGLSFLTVLVLYPSDEGEKISTSVLSITVFLLVIEEIIIPSSSKVIP 294

QY      312 LIGEYLFTMI FTVLSIMVTVPAINIHRRSSSTHNAPLVRKIFLHTLPKLCLMESHVD 371
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      295 LIGEYLLFTMI FTVLSIIVTFVINVHRSSSTTHPAPWPVKRLFLOKLPKLCKMDHVD 354

QY      372 RYFT-QKEETES-----GSGPKSSRNTLEAALNSIRYITRHIMKENDVRE 415
       || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      355 RYSSPEKESQPWWGVKXKKQKSLSDGEKVLAFLKAAADSIRYISRHVKKHFISQ 414

QY      416 VVEDWKFAOVLDRMFALTFTFLVFSIVSGLGFVPVVIYKW 454
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      415 VVQDWKFVAQVLDRIFLMFLFLIVSATGSLVLIPTALKOMW 453


RESULT 5
US-08-484-722-4
; Sequence 4, Application US/08484722
; Patent No. 6485967
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,722
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9952
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-722-4

Query Match          64.4%; Score 1582; DB 4; Length 458;
Best Local Similarity 65.8%; Pred. No. 7.3e-161;
Matches 302; Conservative 62; Mismatches 67; Indels 28; Gaps 5

QY      13 LLILLVLVACRGCGLAGAGCAQRGLSEPPSSIAKHEDSLIKOLFODYERWRVPVHLNDKI 72
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      6 MLVLIVL-----GISSATTGF--NSTAENEDALLRHLFGYQKRWFPVHLNDTI 54

QY      73 KTKFGLAISQLVDVEKKQLMTTNVWLKQEWIDVKLRWNPDYGGIKVIRPDSVWTPTD 132
       ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

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Query Match 48.9%; Score 1201.5; DB 1; Length 529;
Best Local Similarity 50.5%; Pred. No. 6.3e-120;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRVPEHLNDKIKIKFGLAISQLVDVDE 88
DB 41 LSSPPTALPOGSGHTEDETLFKHLFGYNRWARPVNTSDVIVRFGLSIAQLDVIDE 100
QY 89 KNQMTTNVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLFDNADGREGT-S 147
DB 101 KNQMTTNVWLKQESDYKLRWNPADFGNITSIRVPSSEMIWIPDIVLYNNADGEFAVTHM 160
QY 148 TKTIVRYNGTVTWTTPPANKYSCCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
DB 161 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQCNCKMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPVYTVSFVIRKRLPLFYTLFLIIPCIGLS 265
DB 221 DLKDYWESGEWAI VNAATGTYNSKKYDCCAEIYPDVYAFVIRRLPFTYINLIIFCLLIS 280
QY 266 FLTVLVFLYLPNSGEKICLCTSVLVSFTVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVT 325
DB 281 CLTVLVFLYLPSCGCKITLCISVLLSLTVFLLITEIIPSTSLVPLIGEYLLFTMIFVT 340
QY 326 LSIWTVFPAINIHRRSSSTHNAAPLVKIFLHTLPKLLCM----- 366
DB 341 LSIWTVFVNLVNHRRSPSTH-TMPHWVRGALLGCVPRMLLMNRPPPPVELCHPLRLKLSLP 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
DB 400 SYHMLNSVDAEEREVEEEDRWACAGHAPSVGTLCSHGHLHSGASGPKAEALLQGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDREVVEDWKFIAQVLDRLMFLTFVSVIGSLGL 446
DB 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWYVAMVIDRIFLWFIIVCFGLTIGL 519
QY 447 FVP 449
DB 520 FLP 522

RESULT 7

US-08-487-596-2
; Sequence 2, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-596-2

Query Match 48.9%; Score 1201.5; DB 4; Length 529;
Best Local Similarity 50.5%; Pred. No. 6.3e-120;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRVPEHLNDKIKIKFGLAISQLVDVDE 88
DB 41 LSSPPTALPOGSGHTEDETLFKHLFGYNRWARPVNTSDVIVRFGLSIAQLDVIDE 100
QY 89 KNQMTTNVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLFDNADGREGT-S 147
DB 101 KNQMTTNVWLKQESDYKLRWNPADFGNITSIRVPSSEMIWIPDIVLYNNADGEFAVTHM 160
QY 148 TKTIVRYNGTVTWTTPPANKYSCCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
DB 161 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQCNCKMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPVYTVSFVIRKRLPLFYTLFLIIPCIGLS 265
DB 221 DLKDYWESGEWAI VNAATGTYNSKKYDCCAEIYPDVYAFVIRRLPFTYINLIIFCLLIS 280
QY 266 FLTVLVFLYLPNSGEKICLCTSVLVSFTVFLVIEEIIIPSSSKVPIPLIGEYLVFTMIFVT 325
DB 281 CLTVLVFLYLPSCGCKITLCISVLLSLTVFLLITEIIPSTSLVPLIGEYLLFTMIFVT 340
QY 326 LSIWTVFPAINIHRRSSSTHNAAPLVKIFLHTLPKLLCM----- 366
DB 341 LSIWTVFVNLVNHRRSPSTH-TMPHWVRGALLGCVPRMLLMNRPPPPVELCHPLRLKLSLP 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
DB 400 SYHMLNSVDAEEREVEEEDRWACAGHAPSVGTLCSHGHLHSGASGPKAEALLQGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDREVVEDWKFIAQVLDRLMFLTFVSVIGSLGL 446
DB 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWYVAMVIDRIFLWFIIVCFGLTIGL 519
QY 447 FVP 449
DB 520 FLP 522

RESULT 8

US-08-660-451A-2
; Sequence 2, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:

APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NUCLEAR NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-660-451A-2

Query Match 48.9%; Score 1201.5; DB 4; Length 529;
Best Local Similarity 50.5%; Pred. No. 6.3e-120;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
37 LSPSSIA-----KHEDSLKDLFQDYERWVRPVEHLNDKIKFGLAISQVVDVE 88
41 LSPSPALPQGGSHTEBRLFKHLFGYNRWARPVNTSDVIVRFGLSIAQLIDVE 100
89 KNQLMTNVMLKQEWIDVKLRWNPDDYGGIKVIRVPSDVWTPDIVLFDNADRGFECT-S 147
101 KNQMTNVMLKQWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGEFATM 160
148 TKTVIRVNGVTWTPPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYGQSDVILLEDQDV 207
161 TKHLFTGTGVHWVPPAIYKSSCIDVTFPPFDQNCMKFGSWTYDKAKIDLEQMEQTV 220
208 DKRDFDNGEWEIVSATSNGNRDSCC--WYPVVTYSFVKRLPLFVTLFLIIPCIGLS 265
221 DLKQWESGWAIVNATGTNYSKYDCAEYIPDVYAFVIRRLPFTYTLNLIIPCLLIS 280
266 FLTIVFLYPSNEGEKICLCTSVLSVTLVFLVIEEIPSSKVIPIGELYVFTMIFVT 325
281 CLTVLVFLYSDCGEKITLCISVLLSLTVFLLLITEIIPSTLSVPIPIGELYVFTMIFVT 340
326 LSIWTVFAINIHRSSSTNNAPLVKRIPLHTLPKLLCM----- 366
341 LSVITVFLVNLVHRRSPSTH--TMPHWVRGALLGCVPRMLLMNRPPPVLPCHLRLKSP 399

367 -----RSHVD---RYFTQKBE-----ESGSGPKSS----- 389
400 SYHLESNDVAERREVVVEEDRWACAGHVAPSGTLCSHGLHSGASGPKAALLQEGE 459
390 ---RNTLEALNSIRVITHIMKENDVREVVEDMKFTAOVLDRMFLWTFVLSVGL 446
460 LLSPHMQALEGVHYIADHLRSEDADSSVKEDMKVAMVIDRFLWFLFIIVCFGLTIGL 519
447 FVP 449
520 FLP 522
RESULT 9
US-08-464-258B-4
Sequence 4, Application US/08464258B
Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-258B-4

Query Match 48.0%; Score 1179; DB 3; Length 511;
Best Local Similarity 49.0%; Pred. No. 1.5e-117;
Matches 235; Conservative 70; Mismatches 107; Indels 68; Gaps 6;
37 LSPSSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKFGLAISQVVDVDEKQLMTTN 96
26 LQQGSHTHAEDRLFKHLFGYNRWARPVNTSDVIVRFGLSIAQLIDVDEKQMMTN 85
97 VWLKQEWIDVKLRWNPDDYGGIKVIRVPSDVWTPDIVLFDNADRGFECT-STKTVIRYN 155
86 VWLKQEWIDVKLRWNPDDYGGIKVIRVPSDVWTPDIVLFDNADRGFECT-STKTVIRYN 145
156 GTVTVTPPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYGQSDVILLEDQDVDRKDFDN 215

Db 146 GTVHWPPAIYKSSCIDVTFPPFDOONCKMFGSWTYDKAKIDLEQMERTVDLDKYWES 205
QY 216 GEWEIVSATGSKNRTDSCC--WYPVYTVSVFVIRKPLPFTLFLIIPICIGLSFLTVLVPY 273
Db 206 GEWAIIATGTVNSKKYDCCABIIYDPVTVYFVIRRLPFTLFLIIPICIGLSFLTVLVPY 265
QY 274 LPSNEGEKICICTSVLSLTVFLVIEEIIIPSSKVIPLIGYLVFTMIFVLSIMVTVF 333
Db 266 LPSECEGEKITLCSVLLSLTVFLVIEEIIIPSTSLVPLIGBYLLFTMIFVLSIVTVF 325
QY 334 AINIHRRSSSTHNAAPLVRKIFLHTLPKLLCWRSHV----- 370
Db 326 VLVNHRSPSTH--MNVWRVALLGRVPRWLLMNRPLPMLHSGPDLKLSPSYHWLETN 384
QY 371 ----DRTYFQKEETSGSG-----PKSSRNTL----- 393
Db 385 MDAGEREEETEEBEEEDENICVAGLPDSSMGVLYGHGGLHURAMEPETKPSQASEILL 444
QY 394 ----BAALNSIRYITRHMKNENDVREVVEDWKFIAQVLDRLMFLWTFVLSVIGSLGLFVP 449
Db 445 SPOIKALEGVHYIADRLSEADSSVKEDWKYVAMVVDRIEFLWLFIIVCFLGTIGLFLP 504

RESULT 10

US-08-466-589-2

; Sequence 2, Application US/08466589

; Patent No. 5837489

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClaim

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: Fast-SEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,589

; FILING DATE: June 5, 1995

; CLASSIFICATION: 536

; PRIOR APPLICATION NUMBER:

; FILING DATE: March 8, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-9950

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-238-0599

; TELEFAX: 619-238-0062

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 528 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-466-589-2

Query Match

Best Local Similarity 47.6%; Score 1169; DB 2; Length 528;

Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVAPVEHLNDKIKIKFGLAISQLVDVDE 88
Db 41 LSSPSPALPOGSGSHTEDERLFHLFRGYNRWARPEVNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KNOLMTTNWLKOEWDVKLRNPPDYGKIVIRVPSDSVWTPDIVLFDNADRGTEGT-S 147
Db 101 KNQMTTNWLKQESDYKLRNPPADFGNITSLRVPSEMIWIPDIVLY-NXKGEFAVTHM 159
QY 148 TKTVIRYNGTVTWTTPANYKSSCTIDVTFFPFDLQNCMKFGSWTYDGSQVDI ILEDQDV 207
Db 160 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFFPFDQNCMKFGSWTYDKAKIDLEQEQV 219
QY 208 DKRDFDNGEWBIIVSATGSKNRTDSCC--WYPVYTVSVFVIRKPLPFTLFLIIPICIGLS 265
Db 220 DLKDYWSEGEWAIVNATGYNSKKYDCCAEIYDPVTVYAFVIRRLPFTLFLIIPICLLIS 279
QY 266 FLTVLAVFVLPNSGEKICICTSVLSLTVFLVIEEIIIPSSKVIPLIGYLVFTMIFV 325
Db 280 CLTVLAVFVLPNSGEKICICTSVLSLTVFLVIEEIIIPSTSLVPLIGYLVFTMIFV 339
QY 326 LSIMVTVEFAINIHRRSSSTHNAAPLVRKIFLHTLPKLLCM----- 366
Db 340 LSIVITVFLVNDHRSPTH--TMPHWVRGALLGCVPRLWLLMNRPPPVVELCHPLRLKLS 398
QY 367 ----RSHVD--RYFTQKEET-----BSSGSPKSS----- 389
Db 399 SYHLESNVDAEEREVVVEEDRWACAGHAPSVGTLCSHGHLHSGAGPKAEALLQE 458
QY 390 ---RNTLEAALNSIRYITRHMKNENDVREVVEDWKFIAQVLDRLMFLWTFVLSVIGSLGL 446
Db 459 LLLSPHMQALEGVHYIADRLSEADSSVKEDWKYVAMVVDRIEFLWLFIIVCFLGTIGL 518
QY 447 FVP 449
Db 519 FLP 521

RESULT 11
US-08-700-636-2
; Sequence 2, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-700-636-2

Query Match 47.6%; Score 1169; DB 2; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSPSSIA-----KHEDSLKDLFQDYERWRVVEHLNDKIKFKGLAISQLVDVDE 88
DB 41 LSPSPALPQGGSHTEDELFKHLFRGNRWARPVNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KNQLMTTNVWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVMTDPDVLFDNADRFECT-S 147
DB 101 KNQMTTNVWLKQEWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLY-NKXGEFAVTHM 159
QY 148 TKTIVIRNGTVTPPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDILEDDV 207
DB 160 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQONCKMKFGSWTYDKAKIDLEQMEQTV 219
QY 208 DKRDFPDNGEWEIVSANGSKGNRTDSC--WYPVTVYSFVIRKPLFLYTLFLIIPCIGLS 265
DB 220 DLKDYWESGEWAIWVATGTVNSKYDCCAEIYPDVTVAFVIRRLPLFYTLINLIIPCLIS 279
QY 266 FLTIVLFPYPSNEGEKICLCTSVLVSITVFLVIEEIPSSKVIPIGELYVFTMIFVT 325
DB 280 CLTVLVPYLPSCGCKITLCISVLSLTVFLLIITEIPSTSLVPIGELYVFTMIFVT 339
QY 326 LSIMVTVFAINIHRSSSTHNAAPLVKIFLHTLPKLLCM-----ESGSGPKSS 366
DB 340 LSVITVFLVNDVHRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPPPVELCHPLRLKLSLSP 398
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS 389
DB 399 SYHWLESNDVDAEREVVVEEDRWACAGHVPASVGTLCSHGHLHSGASGPKAALLQGE 458
QY 390 ---RNTLEAALNSIRYITRHKENDVREVEDWKFAQLVDRMFLWTFVSVIGSLGL 446
DB 459 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMWIDRIFLWFLFIIVCFGLTIGL 518
QY 447 FVP 449
DB 519 FLP 521

RESULT 12
US-08-467-574-2
Sequence 2, Application US/08467574
Patent No. 6022704
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-467-574-2

Query Match 47.6%; Score 1169; DB 3; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSPSSIA-----KHEDSLKDLFQDYERWRVVEHLNDKIKFKGLAISQLVDVDE 88
DB 41 LSPSPALPQGGSHTEDELFKHLFRGNRWARPVNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KNQLMTTNVWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVMTDPDVLFDNADRFECT-S 147
DB 101 KNQMTTNVWLKQEWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLY-NKXGEFAVTHM 159
QY 148 TKTIVIRNGTVTPPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDILEDDV 207
DB 160 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQONCKMKFGSWTYDKAKIDLEQMEQTV 219
QY 208 DKRDFPDNGEWEIVSANGSKGNRTDSC--WYPVTVYSFVIRKPLFLYTLFLIIPCIGLS 265
DB 220 DLKDYWESGEWAIWVATGTVNSKYDCCAEIYPDVTVAFVIRRLPLFYTLINLIIPCLIS 279
QY 266 FLTIVLFPYPSNEGEKICLCTSVLVSITVFLVIEEIPSSKVIPIGELYVFTMIFVT 325
DB 280 CLTVLVPYLPSCGCKITLCISVLSLTVFLLIITEIPSTSLVPIGELYVFTMIFVT 339
QY 326 LSIMVTVFAINIHRSSSTHNAAPLVKIFLHTLPKLLCM-----ESGSGPKSS 366
DB 340 LSVITVFLVNDVHRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPPPVELCHPLRLKLSLSP 398
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS 389
DB 399 SYHWLESNDVDAEREVVVEEDRWACAGHVPASVGTLCSHGHLHSGASGPKAALLQGE 458
QY 390 ---RNTLEAALNSIRYITRHKENDVREVEDWKFAQLVDRMFLWTFVSVIGSLGL 446
DB 459 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMWIDRIFLWFLFIIVCFGLTIGL 518
QY 447 FVP 449
DB 519 FLP 521

RESULT 13
US-09-217-345-2
Sequence 2, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehmman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-217-345-2

Query Match 47.6%; Score 1169; DB 4; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;
QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQLVDVDE 88
DB 41 LSSPSPTALPGGSHTEEDRLFKHLFGYNEWRPVPNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KQLMTTNVWLKQEWIDVKLRNPDYGGIKVIRVPSDSVMTDPDVLFDNADGRFGT-S 147
DB 101 KNQMTTNVWLKQESDYKLRNPDGNTSLRVPSEMIWIPDIVLY-NKKGEFVTHM 159
QY 148 TKTVIRNGTVTTPPANKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
DB 160 KRAHFLSTGTVHVWPATYKSSCSIDVTFPPDLQNCMKFGSWTYDQAKIDLEQMTV 219
QY 208 DKRPFDNGEIVSATSGKNRDSCC-WPYVTVYSFVTKRLPLFTFLIIPICGLS 265
DB 220 DLKDYWESGEWALVNAATYNSKKYDCAEYIPDVTYAFVIRRLPLFTINLIIPCLLS 279
QY 266 FLTVLVFLPSNEGKICLCTSVLSVLTFLVLLVIBEEIIPSSSKVLIPLIGEYLVFTMIVT 325
DB 280 CLTVLFLVFLPSDCGKICLCTSVLSVLTFLVLLVIBEEIIPSTSLVPLIGEYLVFTMIVT 339
QY 326 LSIWTVTFAINHHRSSSTHMAPLVKIFLHTLPKLLCM----- 366
DB 340 LSIWTVTFAINHHRSSSTHMAPLVKIFLHTLPKLLCM----- 366
QY 340 LSIWTVTFAINHHRSSSTHMAPLVKIFLHTLPKLLCM----- 366
DB 340 LSIWTVTFAINHHRSSSTHMAPLVKIFLHTLPKLLCM----- 366

QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
DB 399 SYHWLESNVDAEEREVVVEEDRWACAGHAPSVGTLCSHGHLHSGAGSPKAEALLQGE 458
QY 390 ---RNTLEAALNSIRYITRHTMKENDVREVVEDKFKIAQVLDRLMFLTWFLFVSVIGSLGL 446
DB 459 LLLSPHMQKALEGVHYIADHLRSBADSSVKEDWKYVAMVDRIFLWLFIIIVCFILGTGL 518
QY 447 FVP 449
DB 519 FLP 521
RESULT 14
US-08-278-635B-4
; Sequence 4, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 8
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-4

Query Match 47.6%; Score 1168.5; DB 1; Length 510;
Best Local Similarity 48.6%; Pred. No. 2.1e-116;
Matches 233; Conservative 71; Mismatches 108; Indels 67; Gaps 6;
QY 37 LSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQLVDVDEKQLMTTN 96
DB 26 LTQOGSHAEADRLFKHLFGYNEWRPVPNTSDVIVRFGLSIAQLIDVDEKQLMTTN 85
QY 97 VWLQKQEWIDVKLRNPDYGGIKVIRVPSDSVMTDPDVLFDNADGRFGT-STKTIVRYN 155
DB 86 VWLQKQEWIDVKLRNPDYGGIKVIRVPSDSVMTDPDVLFDNADGRFGT-STKTIVRYN 145
QY 156 GTVWTPPANKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDVDRKDPDN 215
DB 146 GTVWTPPANKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDVDRKDPDN 205

Result No.	Query No.	Score	Query			DB ID	Description
			Match	Length	DB		
1	2456	100.0	468	18	AAW09024	Neuronal nicotinic	
2	2456	100.0	468	23	ABB82433	Human neuronal NAC	
3	2456	100.0	468	23	ABG70480	Human neuronal nic	
4	1586	64.6	458	18	AAW09020	Neuronal nicotinic	
5	1586	64.6	458	22	AAE12775	Human cholinergic	
6	1582	64.4	458	23	ABB82437	Human neuronal NAC	
7	1582	64.4	458	23	ABG70494	Human neuronal nic	
8	1201.5	48.9	529	15	AAW44155	Human neuronal nic	
9	1201.5	48.9	529	16	AAR73966	Alpha 2 subunit of	

SUMMARIES

PT used in screening to det

PT used in screening to det

XX Human neuronal nicotinic acetylcholine receptor alpha 5 subunit.
 XX Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
 KW ion flux; alpha 5 subunit.
 XX Homo sapiens.
 XX US6440681-B1.
 XX 27-AUG-2002.
 XX 07-JUN-1995; 95US-0487596.
 XX 03-APR-1990; 90US-0504455.
 XX 30-NOV-1992; 92US-0938154.
 XX 08-MAR-1993; 93US-0028031.
 XX 08-NOV-1993; 93US-0149503.
 XX (MERI) MERCK & CO INC.
 XX PA Elliott KJ, Ellis SB, Harpold WM;
 XX PI WPI: 2002-711528/77.
 XX DR N-PSDB; ABS54873.
 XX XX
 XX Identifying antagonists or agonists of human neuronal nicotinic
 PT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 PT nAChR -
 XX
 XX Claim 118; Column 49-52; 56pp; English.
 XX The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nAChRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nAChR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nAChR (alpha or beta) subunit, such that the cells express an
 CC nAChR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents the alpha 5 subunit of the human nAChR
 CC polypeptide.
 XX
 XX Sequence 468 AA;
 SQ

Query Match 100.0%; Score 2456; DB 23; Length 468;
 Best Local Similarity 100.0%; Pred. No. 7.6e-231;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARGSGPRALRLLLLVOLVAGRCGLAGAGGAQGLSEPPSSIAKHEDSLKDLFDYER 60
 DB 1 MAARGSGPRALRLLLLVOLVAGRCGLAGAGGAQGLSEPPSSIAKHEDSLKDLFDYER 60
 QY 61 WVRPVEHLNDKIKIFGLAISQLVDVDEKNQLMTTNVWLKQEWIDVLRWNPDDYGGIKV 120
 DB 61 WVRPVEHLNDKIKIFGLAISQLVDVDEKNQLMTTNVWLKQEWIDVLRWNPDDYGGIKV 120
 QY 121 IRVPSDSVWTPDIVLFDNADGRFEGTSTKTVIRYNGTWTWPPANYKSSCTIDVTFPPFD 180
 DB 121 IRVPSDSVWTPDIVLFDNADGRFEGTSTKTVIRYNGTWTWPPANYKSSCTIDVTFPPFD 180
 QY 181 LQNCMSKFGSWTYDCGSQVDIILEDQVDKDPFDNGEWEIVSATSGKGRNRTDSCCWYPV 240
 DB 181 LQNCMSKFGSWTYDCGSQVDIILEDQVDKDPFDNGEWEIVSATSGKGRNRTDSCCWYPV 240
 QY 241 TYSFVIRKLPFLPYTLFLIPIGSLFTLVLPYLPSEGEKICICTSVLVSITVFLLVIE 300
 DB 241 TYSFVIRKLPFLPYTLFLIPIGSLFTLVLPYLPSEGEKICICTSVLVSITVFLLVIE 300
 QY 301 EIIPSSKVIPIGLSYLVFTMI FVTLTSMVTVFAINIHRSSSTHNAPLVRKIFLHTL 360
 DB 301 EIIPSSKVIPIGLSYLVFTMI FVTLTSMVTVFAINIHRSSSTHNAPLVRKIFLHTL 360

QY 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHMKENDVREVVEDW 420
 DB 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHMKENDVREVVEDW 420
 QY 421 KFAIQVLDRLMFLWTFLFVSIVGSLGLFVPVVIYKWNILIPVHIGNANK 468
 DB 421 KFAIQVLDRLMFLWTFLFVSIVGSLGLFVPVVIYKWNILIPVHIGNANK 468

RESULT 4

AAW09020
 ID AAW09020 standard; Protein; 458 AA.

XX AC AAW09020;

XX DT 09-APR-1997 (first entry)

XX DE Neuronal nicotinic acetylcholine receptor beta-3 subunit.

XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 ligand-gated receptor.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..20

XX FT Domain /label= Sig_peptide

XX FT /label= TMD1

XX FT /note= "transmembrane domain 1"

XX FT /label= TMD2

XX FT /note= "transmembrane domain 2"

XX FT /label= TMD3

XX FT /note= "transmembrane domain 3"

XX FT /label= TMD4

XX FT /note= "transmembrane domain 4"

XX PN WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold WM;

XX DR WPI: 1997-065463/06.

XX DR N-PSDB; AAT48234.

XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 used in screening to determine the effect of drugs on the receptor

XX Claim 12; Page 79-81; 108pp; English.

XX The amino acid sequence (AAW09020) of the beta-3 subunit of the
 human neuronal nicotinic acetylcholine receptor (nAChR) was deduced
 from a DNA clone (AAT48234) isolated from a human substantia nigra
 cDNA library. Recombinant beta-3 subunits can be expressed in host
 cells, esp. mammalian cells or amphibian oocytes, optionally with
 alpha-2, alpha-3, alpha-4, alpha-5, alpha-6 and/or alpha-7 subunits
 (see also AAW09018-19, AAW09021-25). The recombinant subunits and host
 cells can be used to study the function of the human nAChR and to
 identify cpds. that modulate its activity.

DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
 XX Human nAChR; neuronal nicotinic acetylcholine receptor;
 KW neurotransmitter.

OS Homo sapiens.

XX WO9513299-A1.

XX PD 18-MAY-1995.

XX PF 08-NOV-1994; 94WO-US12859.

XX PR 08-NOV-1993; 93US-0149503.

XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI Elliott KJ, Ellis SB, Harpold MM;

XX DR WPI; 1995-194036/25.

XX DR N-PSDB; AAQ90387.

XX New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA
 PT used to develop prods. for detection, diagnosis and therapy and for
 PT modulating activity

XX PS Disclosure; Page 43-46; 54pp; English.

XX DNA encoding the human nAChR alpha2 subunit was isolated from a
 CC human thalamus tissue cDNA library using corresp. rat cDNA. The
 CC insert of one clone obtd. was ligated with the insert of another
 CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
 CC used to identify function nAChRs. Cells contg. the DNA can be used
 CC for screening to identify cpds. which modulate the activity of human
 CC nAChRs. The human nAChR alpha 2 subunit can be used to product
 CC antibodies which can be used in immunostochemistry, diagnosis and
 CC therapy. The nucleic acids can be used for analysing disease states
 CC and creating animal models.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 529 AA;

Query Match 48.9%; Score 1201.5; DB 16; Length 529;
 Best Local Similarity 50.5%; Pred. No. 3.2e-108;
 Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFDYERWVRPVEHLNDKIKIFGLAISQLVDYDE 88
 DB 41 LSSPSPALPOGSGSHSTEDRLFKHLFRGYNRWARPVPNTSDVIVRFGLSIAQLIDYDE 100
 QY 89 KNQMTTNVWLKQEWIDVKLRNPDYGGIKVIRVPSDSVTPDVLFDNADGRPEGT-S 147
 DB 101 KNQMTTNVWLKQESDYKLRNPDAGFNITSLRVPSEMIWIPDVLVYNNADGEFAVTHM 160
 QY 148 TKTIVRYNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
 DB 161 TKAHLFSTGTVHWVPPAIYKSSCIDVTFPPDQNCMKFGSWTYDQAKIDLSQMEQTV 220
 QY 208 DKRDPDNGEWEIVSATSGKNRTDSC--WYPVTVYSFVIKRLPFLTLIIPICGLS 265
 DB 221 DLKDYWESGEWAI VNAVTGYSKDYCCAEIYDPDVTYAFVIRRLPFLTYINLIIPCLLIS 280
 QY 266 FLTVLVFLYLPNNEGKICLCTSVLSLVFLVILLVIEEIIIPSSKVIPLIGELVFTMIFVT 325
 DB 281 CLTVLVLFPDQCGKIKLCTSVLSLVFLVILLVIEEIIIPSTLSVLIPLIGELVFTMIFVT 340
 QY 326 LSIWTVFPAIINHRSSTTHNAPLVRKI FLHTLPKLLCM----- 366
 DB 341 LSIWTVFVNLVHHSPSTH-TMHWVRGALIGCVPRWLLNMRPPPPVELCHPLRLKLS 399
 QY 367 -----RSVD---RYFTQKEET-----BSGGPKSS----- 389
 DB 400 SYHWLESNVDAEEVVVEEDRWACAGHAPSVGTCLSGHGLHSGAGSPKAEALLQGE 459

QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIQAQVLDRLMFLWTFLFVSIYVGLGL 446
 DB 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIIVCFPLGTIGL 519
 QY 447 FVP 449
 DB 520 FLP 522

RESULT 10

AAW09021
 ID AAW09021 standard; Protein; 529 AA.

XX AC AAW09021;

XX DT 09-APR-1997 (first entry)

XX DE Neuronal nicotinic acetylcholine receptor alpha-2 subunit.

XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.

XX OS Homo sapiens.

XX PN WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold MM;

XX DR WPI; 1997-065463/06.

XX DR N-PSDB; AAT48235.

XX PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 PS Disclosure; Page 49-52; 108pp; English.

XX The alpha-2 subunit (AAW09021) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transformed
 CC host cells carrying alpha-2 subunit DNA (see also AAT48235). Host
 CC cells, esp. mammalian cells or amphibian oocytes, expressing the
 CC recombinant alpha-2 subunit, opt. in combination with other
 CC recombinant alpha and/or beta subunits (see also AAW09018-20,
 CC AAW09022-27) can be used to examine the function of human AChR and
 CC to identify cpds. that modulate its activity.

XX Sequence 529 AA;

Query Match 48.9%; Score 1201.5; DB 18; Length 529;
 Best Local Similarity 50.5%; Pred. No. 3.2e-108;
 Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFDYERWVRPVEHLNDKIKIFGLAISQLVDYDE 88
 DB 41 LSSPSPALPOGSGSHSTEDRLFKHLFRGYNRWARPVPNTSDVIVRFGLSIAQLIDYDE 100
 QY 89 KNQMTTNVWLKQEWIDVKLRNPDYGGIKVIRVPSDSVTPDVLFDNADGRPEGT-S 147
 DB 101 KNQMTTNVWLKQESDYKLRNPDAGFNITSLRVPSEMIWIPDVLVYNNADGEFAVTHM 160
 QY 148 TKTIVRYNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
 DB 161 TKAHLFSTGTVHWVPPAIYKSSCIDVTFPPDQNCMKFGSWTYDQAKIDLSQMEQTV 220
 QY 208 DKRDPDNGEWEIVSATSGKNRTDSC--WYPVTVYSFVIKRLPFLTLIIPICGLS 265

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Db 221 DLKDYWESGEWAIIVNATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTNLIIPCLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLSVLTVPFLVLEEIIIPSSKVIPLIGEVLFVTMIFVT 325
Db 281 CLTVLVFLPSDCGEKITLCISVLSTVFLLLITEIIPSTSLVPLIGEVLFVTMIFVT 340
QY 326 LSIIMVTFAINIHRSSSTHNAAPLVKIFLHTLPKLLC----- 366
Db 341 LSIIVITVFLNVHRSPTH-TMFWVRGALLGCVPRLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
Db 400 SYHWLESNVDAEREVVVEEDRWACAGHVAPSVGTLCSHGLHSGASGPKAEALLQEGE 459
QY 390 ---RNTLEAALNSTRYITRHKENDVREVVEDWKFIAQVLDRLMFLWTLFVSIVGSLG 446
Db 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWFLFIIVCFLGTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 11
ID ABB82430
AC ABB82430;
XX 22-JAN-2003 (first entry)
XX Human neuronal NACHR alpha2 subunit.
XX Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
XX immunochemistry; NACHR alpha2 subunit; receptor.
XX Homo sapiens.
XX W0200259266-A2.
XX 01-AUG-2002.
XX 29-OCT-2001; 2001WO-US0985.
XX 01-NOV-2000; 2000US-0703951.
XX (MERI ) MERCK & CO INC.
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
XX WPI; 2002-698532/75.
XX N-PSDB; ABV73243.
XX Cell comprising nucleic acids encoding human alpha and beta subunits of
XX neuronal nicotinic acetylcholine receptors, useful for in vitro
XX screening of a drug substance in a test system specific for humans -
XX Examples; Page 111-113; 143pp; English.
XX The invention relates to a suitable host cell transfected with an
XX isolated nucleic acid molecule comprising a sequence of nucleotides or
XX ribonucleotides that encodes at least one alpha or beta subunit of a
XX human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
XX and methods of the present invention, which provide a means to prepare
XX synthetic or recombinant receptors and receptor subunits that are
XX substantially free of contamination from many other receptor proteins,
XX are useful for observing the effect of a drug substance on a particular
XX subtype to perform in vitro screening of the drug substance in a test
XX system that is specific for humans. The antibodies can be used in
XX immunochemistry and for diagnostic and therapeutic applications. The
XX present sequence represents a human neuronal NACHR alpha2 subunit.
XX

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SQ Sequence 529 AA;
Query Match 48.9%; Score 1201.5; DB 23; Length 529;
Best Local Similarity 50.5%; Pred. No. 3.2e-108;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRVPEHLNDKIKIKFGLAISQDVDE 88
Db 41 LSEPSPTALPQGGSHTEDETRFLFKLFRGYNRWARPVPNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KQQLMTNINWLVKQEWIDVKLRWNPDDYGGIKVIRVSDSVWTPDIVLFDNADGRFSGT-S 147
Db 101 KQOMTNTNWLKQEWSDYKLRWNPADFGNITSIRVFSMIWIPIDIVLYNNADGEFAVTHM 160
QY 148 TKTIVRYNGTVTTPPANYKSSCTIDVTFPPDLQNSMKFGSWTYDGSQVDIILEDDQV 207
Db 161 TKAHLESTGTVHWVPAIYKSSCIDVTFPPDQCNCKMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATSGKNRDTSCC--WYPVYTVSFVIRKPLPLFYTLFLIIPICIGLS 265
Db 221 DLKDYWESGEWAIIVNATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTNLIIPCLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLSVLTVPFLVLEEIIIPSSKVIPLIGEVLFVTMIFVT 325
Db 281 CLTVLVFLPSDCGEKITLCISVLSTVFLLLITEIIPSTSLVPLIGEVLFVTMIFVT 340
QY 326 LSIIMVTFAINIHRSSSTHNAAPLVKIFLHTLPKLLC----- 366
Db 341 LSIIVITVFLNVHRSPTH-TMFWVRGALLGCVPRLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
Db 400 SYHWLESNVDAEREVVVEEDRWACAGHVAPSVGTLCSHGLHSGASGPKAEALLQEGE 459
QY 390 ---RNTLEAALNSTRYITRHKENDVREVVEDWKFIAQVLDRLMFLWTLFVSIVGSLG 446
Db 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWFLFIIVCFLGTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 12
ABG31800
ID ABG31800 standard; Protein; 529 AA.
XX AC ABG31800;
XX 06-DEC-2002 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha 2 subunit.
XX Human; neuronal nicotinic acetylcholine receptor; nNACHR; receptor;
XX ion flux; alpha 2 subunit.
XX Homo sapiens.
XX US6440681-B1.
XX 27-AUG-2002.
XX 07-JUN-1995; 95US-0487596.
XX 03-APR-1990; 90US-0504455.
XX 30-NOV-1992; 92US-0938154.
XX 08-MAR-1993; 93US-0028031.
XX 08-NOV-1993; 93US-0149503.
XX (MERI ) MERCK & CO INC.
XX Elliott KJ, Ellis SB, Harpold MM;
XX

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Db 221 DLKDYWESGEWAIWATGTNTSKYCCABYDVTVAFVIRLPLFYTNILIPCLLIS 280
QY 266 FLTVLFLPSNKEGKICLCTSVLSLTVELLVEEIPSSKVIPLIGLYLFTMIFVT 325
Db 281 CLTVLFLPSDCEKICLCTSVLSLTVELLVEEIPSSKVIPLIGLYLFTMIFVT 340
QY 326 LSIWTVFAINIHRSSTNNAPLVRKIFLHTLPKLLCM----- 366
Db 341 LSIWTVFAINIHRSSTNNAPLVRKIFLHTLPKLLCM----- 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
Db 400 SYHWLESNDVAEREVVVEEDRWACAGHAPSVGTLCSHGHLSGASGPKAALLQEGE 459
QY 390 ---RNTLEAALNSIRYITRIMKENDVREVVEQWKPIAQLVDRMFLWTFVSVGLSL 446
Db 460 LLSLPHMOKALEGVHYIADHLSRSEDADSSVKEDKYYWIDRIFLWFLIIVCFGLTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 14
AAW11824
ID AAW11824 standard; Protein; 627 AA.
XX AC AAW11824;
XX DT 25-MAR-2003 (updated)
XX DT 05-OCT-1997 (first entry)
XX Alpha4 subunit of normal nAChR.
XX nAChR; mutation; autosomal dominant nocturnal frontal lobe epilepsy;
XX ADNFLE; neuronal acetylcholine receptor.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 280
FT /note= "Ser 248 Phe is the ADNFLE-
FT inducing mutation (see AAW11825)"
XX AU9656247-A.
XX 09-JAN-1997.
XX 28-JUN-1996; 96AU-0056247.
XX 28-JUN-1995; 95AU-0003840.
XX (UYBO-) UNIV BONN.
XX (UYME-) UNIV MELBOURNE.
XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
XX Steinlein OK, Mully JC, Propping PJ, Wallace RH, Phillips HA,
XX Sutherland GR, Scheffer IE, Berkovic SF;
XX WPI; 1997-100506/10.
XX DR N-PSDB; AAT59527.
XX CHRNA4 gene encodes neuronal nicotinic acetylcholine receptor
XX fragment - used in diagnosis of autosomal dominant nocturnal frontal
XX lobe epilepsy
XX Disclosure; Fig 13; 20pp; English.
XX The DNA sequence of the normal nAChR is given in AAT59527,
XX the DNA sequence of the ADNFLE-inducing mutant is given in AAT59528.
XX Mutations at codon 248, which have the effect of replacing
XX serine by another amino acid (e.g. phenylalanine) in the sixth
XX amino acid of the transmembrane domain 2 (M2) of the alpha4

CC subunit of nAChR have been found to be associated with ADNFLE.
CC The primers given in AAT59529 and AAT59530 were used in the
CC amplification of part of exon 5.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 627 AA;
Query Match 47.1%; Score 1157.5; DB 18; Length 627;
Best Local Similarity 39.5%; Pred. No. 8.3e-104;
Matches 247; Conservative 77; Mismatches 110; Indels 191; Gaps 8;
QY 7 GPALRLLLVQLVAGRCGLAGAGQAQRLSEPPSIAKHEDSLKDLFQDYRWVRPVE 66
Db 5 GPCAPRLPLPCLLLCT-----GLLRASSHVETRAHAEERLLKLFSGYNKWRPVA 56
QY 67 HLNDKIKIFGLAISQVLDVDEKNQLMTTNVLMKQEMIDVCLRWNPDDVGGIKVIRVPSD 136
Db 57 NSDDVVLVRFGLSIAQLIDVDEKNQMTTNVWVQWHDYKLRWDPADENVTSIRPSE 116
QY 127 SVWTPDIVLFDNADGRFEGTS-TKTIVRYNGTVTTPPPANYKSSCTIDVTFPPFDLQNC 185
Db 117 LIWRPDIVLNNADGDFAVTLTKAHLFHDGRVQMTTPAIYKSSCSIDVTFPPFDQNC 176
QY 186 MKFGSWTYDGSQVDIILEDQDVDRKDFPONGEWEIVSATGSKGNRTDSC--WYPVTYS 243
Db 177 MKFGSWTYDKAKIDLNNHRSRVDQLDFWESGEWIVDAVGTYNTRKYECACAEYDITVA 236
QY 244 FVTKRLPLFVTLFIIPCIIGLSFLTVLVFLPSNEGEKICLCTSVLSLTVELLVEEII 303
Db 237 FVIRRLPLFYTNILIPCLLISCLTVLVFLPSECEKICLCTSVLSLTVELLVEEII 296
QY 304 PSSKVIPLIGLYLFTMIFVTLISIMVTVFAINIHRSSTNNAPLVRKIFLHTLPKL 363
Db 297 PSTSLVPLIGLYLFTMIFVTLISIVTVLVNHHRSRTH-TMPTWVRVRLDIVPRL 355
QY 364 LQWR-----SHVDRYPTQKE----- 378
Db 356 LLMKRPSVVKDNCRRLLIESNMHMASAPRFWEPEGEPPATSGTQSLHPPSPFCVPLDVP 415
QY 379 -----ETESGS----- 384
Db 416 AEPGSPCKSPDQLPPQPLEAKASPHSPGRCRPHGTQAPGLAKARSLVQHMSSPG 475
QY 385 -----GPKSSRNT----- 392
Db 476 EAVEGGVCRSRSIQYCVPRDDAAPEADGQAAGALASRNTSHAELPPDPQSPCKCTCK 535
QY 393 -----LEAALNSIRYITRIMKENDVREVVEQWKPIA 424
Db 536 EPSSVSPSATVKTRSTKAPPPLPLSPALTRAVEGVQYIADHLKABDTDFSVKEDWKYVA 595
QY 425 QVLDRMFLATFLFVSVISGLPLVP 449
Db 596 MVIDRIFLWFIIVCLGTGVGLFP 620

RESULT 15
AAW09023
ID AAW09023 standard; Protein; 627 AA.
XX AC AAW09023;
XX DT 09-APR-1997 (first entry)
XX Neuronal nicotinic acetylcholine receptor alpha-4 subunit.
XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
XX ligand-gated receptor.
XX Homo sapiens.
XX W09641876-A1.
XX

PD 27-DEC-1996.
XX 07-JUN-1996; 96WO-US09775.
XX 07-JUN-1995; 95US-0484722.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Elliott KJ, Harpold MM;
XX WPI; 1997-065463/06.
XX N-PSDB; AAT48237.
XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
PT used in screening to determine the effect of drugs on the receptor
XX Disclosure; Page 58-61; 108pp; English.
XX The alpha-4 subunit (AAW09023) of the human neuronal nicotinic
CC acetylcholine receptor (nAChR) can be expressed in transformed
CC host cells carrying alpha-4 subunit DNA (see also AAT48237). Host
CC cells, esp. mammalian cells or amphibian oocytes, expressing the
CC recombinant alpha-4 subunit, opt. in combination with other
CC recombinant alpha and/or beta subunits (see also AAW09018-22,
CC AAW09024-27), can be used to examine the function of human AChR and
CC to identify cpds. that modulate its activity.
XX Sequence 627 AA;

Query Match 47.1%; Score 1157.5; DB 18; Length 627;
Best Local Similarity 39.5%; Pred. No. 8.3e-104;
Matches 247; Conservative 77; Mismatches 110; Indels 191; Gaps 8;
QY 7 GPRALRLLLLVOLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYERWVRVE 66
DB 5 GPGAPRLPPLLLLT-----GLRASHVETRAHAERLUKLFSGYNKWSRPA 56
QY 67 HLNKDRIKIFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRMNPDDYGGIKVIRVPSD 126
DB 57 NISDVVLVRFGLSIAQLIDVDEKNQMTTNVWLKQEWIDVKLRMNPDDYGGIKVIRVPSD 116
QY 127 SVWTPDIVLFDNADGRPGTS-TKTVIRYNGTVTPPPANYKSSCTIDVTFPPDLQNC 185
DB 117 LIWRPDIIVLYNADGDFATHTLKAHLFDHGRVQWTPPAIYKSSCIDVTFPPDQNC 176
QY 186 MKFGSWTYDGSQVDIILEDQDQVDKDFDNGEWEIVSATGSKNETDSCC--WYPTVYS 243
DB 177 MKFGSWTYDKAKIDVNNHRSRVDQDFWESGEWIVDAVGYNTRKYECCEIYDPIYA 236
QY 244 FVIRKPLPFLYTLPIICIGLSFLVFLVFLPSNEGEKICLCTSVLSLTVFLVIEBII 303
DB 237 FVIRKPLPFLYTLNLIIPCLISCLVFLVFLPSECEKICLCTSVLSLTVFLVIEBII 296
QY 304 PSSKVIPLIGBYLFTMFTVLSIMVTVPAINIHRSSSTHNAAPLVKIFLHTLPKL 363
DB 297 PSTSLVIPLEIGYLLFTMFTVLSIVITVFLNVHRSRPTH-TMPTWVRVFLDIVPRL 355
QY 364 LCMR-----SHVDYFTQKE----- 378
DB 356 LMKRPSVVKONCRRLIESMHKMGASAPRFPWPEGEPPATSGTQSLHPPSPFCVPLDVP 415
QY 379 -----ETESGS----- 384
DB 416 AEPGSKSPDOLPPQPLEAKASPHSPGCPCHPGTQAPGLAKARSLVQHMSPG 475
QY 385 -----GPKSSRNT----- 392
DB 476 EAVEGGRCSRISIQYCVPRDDAAPEADQAGALASRTHSAELPPDPQSPCKCTCK 535
QY 393 -----LEALNSIRYIIRHMKENDVREVWDFIA 424
DB 536 EFSSVSPSATVKTSTRSTKAPPHPLPLSPALTRAEGVQYIADHLKAEDTDFSVKEDWKYA 595

QY 425 QVLDRLMFLWTFLFVSVIVGSLGLFVP 449
DB 596 MVIDRIFLMFIIVCLLGTGVLFLP 620
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: December 23, 2003, 15:35:43 ; Search time 3995 Seconds
(without alignments)
11121.047 Million cell updates/sec

Title: US-09-703-951A-7
Perfect score: 1828
Sequence: 1 CCCGGCGGAGCTGTGGCC.....ATCTAGTATTGTCCTGG 1828

Scoring table: IDENTITY NUC
Gap 10_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
Result No.	Score	Match	Length	ID			
1	718.4	39.3	2449	11	AK080900	AK080900 Mus muscu	
2	608.6	33.3	941	13	B0433768	B0433768 AGNCOURT	
3	593.8	32.5	655	12	BW833917	BW833917 K-EST0116	
4	565.4	30.9	1201	13	BX332469	BX332469 BX332469	

5	521.4	28.5	4589	11	AK030464	AK030464 Mus muscu	
6	505.4	27.6	701	13	B0623054	B0623054 UI-H-Flu1-	
7	505	27.6	527	13	BX107344	BX107344 BX107344	
8	502.2	27.5	713	10	BF793290	BF793290 602252976	
9	493.6	27.0	744	13	BU289501	BU289501 603606675	
10	485.2	26.5	538	9	AV748726	AV748726 AV748726	
11	480.6	26.3	1008	13	BQ932830	BQ932830 AGNCOURT	
12	467.4	25.6	755	10	BF130135	BF130135 601818142	
13	459.4	25.1	542	9	AV749460	AV749460 AV749460	
14	442.4	24.2	858	13	BQ225664	BQ225664 AGNCOURT	
15	433.6	23.7	2257	11	AK017571	AK017571 Mus muscu	
16	431.2	23.6	765	14	CA411814	CA411814 UI-H-E20-	
17	425.2	23.3	496	10	EG185804	EG185804 RST4757 A	
18	421.6	23.1	1280	12	BM465418	BM465418 AGNCOURT	
19	417.4	22.8	918	10	BG216553	BG216553 RST36245	
20	413.8	22.6	655	28	AQ529651	AQ529651 RPCI-11-3	
21	402.2	22.0	597	10	BG080409	BG080409 H3053C09-	
22	396.6	21.7	1194	13	EX394246	EX394246 BX394246	
23	356.8	19.5	604	9	AW390530	AW390530 CMO-ST018	
24	355.2	19.4	495	14	H13022	H13022 Y171F01.r1	
25	352.8	19.3	577	12	BJ058493	BJ058493 BJ058493	
26	344.2	18.8	698	12	BM718981	BM718981 UI-E-E01-	
27	341	18.7	466	14	R19467	R19467 YG21303.r1	
28	340.2	18.6	872	10	BG291447	BG291447 602387329	
29	336	18.4	627	10	BG291359	BG291359 602387229	
30	335.6	18.4	568	12	BI343148	BI343148 371202 MA	
31	325.2	17.8	1071	12	BI522799	BI522799 603175889	
32	321.4	17.6	856	29	CNS04DRH	AL286118 Tetraodon	
33	317.4	17.4	541	12	BM984462	BM984462 UI-CF-DU1	
34	308	16.8	2940	11	AK034228	AK034228 Mus muscu	
35	308	16.8	3230	11	AK083157	AK083157 Mus muscu	
36	302.6	16.6	894	13	BU912419	BU912419 AGNCOURT	
37	296	16.2	564	12	BM035632	BM035632 full8a12.Y	
38	289.4	15.8	326	10	BG199776	BG199776 RST19070	
39	288.6	15.8	659	10	BB645442	BB645442 BB645442	
40	287	15.7	1864	11	AK053497	AK053497 Mus muscu	
41	287	15.7	2916	11	AK051730	AK051730 Mus muscu	
42	287	15.7	3126	11	AK080415	AK080415 Mus muscu	
43	283.2	15.5	854	29	CNS023CO	AL179313 Tetraodon	
44	283.2	15.5	4290	11	AK029177	AK029177 Mus muscu	
45	282.4	15.4	786	29	CNS04J50	AL293085 Tetraodon	

ALIGNMENTS

RESULT 1
AK080900
LOCUS
DEFINITION
AK080900 2449 bp mRNA linear HTC 05-DEC-2002
Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
enriched library, clone:B430203G01 product:NICOTINIC RECEPTOR ALPHA
5 SUBUNIT (FRAGMENT) homolog [Macaca mulatta], full insert
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

AK080900
AK080900.1
GI:26348860
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374

PUBLISHED REFERENCE AUTHORS	11042159 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitasumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4	FEATURES source	Location/Qualifiers 1. .2449 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:B430203G01" /db_xref="taxon:10090" /clone="B430203G01" /sex="male" /tissue_type="adipose" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="4 days neonate" 152. .1243 /note="unnamed protein product; NICOTINIC RECEPTOR ALPHA 5 SUBUNIT (FRAGMENT) homolog [Macaca mulatta] (SPTR) [Q9TUC6, evidence: FASTY, 91.9%ID, 100%length, match=555] putative" /codon_start=1 /protein_id="BAC38070.1" /db_xref="GI:26348861" /translation="MAARGRRRLRLLLVOLLGRWPRPAGARGARDGRPEGAST KTVRVNGVTVTQPNYKSSCTIDVTFPFDLQNCMKFGSWTYDGSODVILEDDQ VRTDPFDNGEWEIMSAGSKNRTDSCWYFCITYSVIKRPLPLETYLFLIPCLGL SFTLVVVFPLPSNEGKISLCTSVLSVLFVLEIEIIPSSKVLPLIGLIVFTMI FVTLSTMTVIFAINIHSSSTNNAMPVRKIFLHKPKLCKMESHADRYFTQREBA EXDGGPKSRNTLEAALDCIRYITRHVVKENDREVVEDWKFIAQLDRMFLMTFLVLS IITGLFLVPVYKWNIIIVPHIGNTIK"
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2449) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216] cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/	BASE COUNT 626 a 558 g 578 G 687 C ORIGIN	Query Match 39.3%; Score 718.4; DB 11; Length 2449; Best Local Similarity 79.7%; Pred. No. 1.5e-129; Matches 875; Conservative 0; Mismatches 216; Indels 7; Gaps 2; 569 GCAGATGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 628 569 GCAGATGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 628 254 GGAGACGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 313 254 GGAGACGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 313 629 ACCTGACCTCCACGGCAAACTACAAAAGTTCTCTGACCATAGATGTCAGCTTTTCCCA 688 629 ACCTGACCTCCACGGCAAACTACAAAAGTTCTCTGACCATAGATGTCAGCTTTTCCCA 688 314 ACTTGACGGACGACCAAACTACAAAAGTTCTTGCACTATAGATGACCTTTTCCCA 373 314 ACTTGACGGACGACCAAACTACAAAAGTTCTTGCACTATAGATGACCTTTTCCCA 373 689 TTTGACCTTCAGAACTGTTTCCATGAAATTTGGTTCTTGGACTTTATGATGATGATGATGATG 748 689 TTTGACCTTCAGAACTGTTTCCATGAAATTTGGTTCTTGGACTTTATGATGATGATGATGATG 748 374 TTTGATCTCCAAATTTGCTCCATGAAATTCGGCTCATGACGATGATGATGATGATGATGATG 433 374 TTTGATCTCCAAATTTGCTCCATGAAATTCGGCTCATGACGATGATGATGATGATGATGATG 433 749 GATATAATTTCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGAG 808 749 GATATAATTTCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGAG 808 434 GATATAATTTCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGAG 493 434 GATATAATTTCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGAG 493 809 GAGATTGTGAGTGCAACAGGACCAAGAAAGCAAGACGACAGCTGTTGCTGATGATGATG 868 809 GAGATTGTGAGTGCAACAGGACCAAGAAAGCAAGACGACAGCTGTTGCTGATGATGATG 868 494 GAAATCATGAGCGCAATGGGAGCAAGGGAACCGGACGACAGCTGCTGCTGCTGCTGCTG 553 494 GAAATCATGAGCGCAATGGGAGCAAGGGAACCGGACGACAGCTGCTGCTGCTGCTGCTG 553 869 TATGTGCACTTACTTACTTCTGTAATCAAGCGCTGCGCTCTCTTCTTATACCTTCTTCTTATA 928 869 TATGTGCACTTACTTACTTCTGTAATCAAGCGCTGCGCTCTCTTCTTATACCTTCTTCTTATA 928 554 TGCATCACCTACTCTCTTCTGATCAACGGCTGCGCTCTCTTCTACACCTGTTTCTTATC 613 554 TGCATCACCTACTCTCTTCTGATCAACGGCTGCGCTCTCTTCTACACCTGTTTCTTATC 613 929 ATACCTGATTTGGGCTCTCAATTTTAACTGTAATGCTTCTTCTTCTTCTTCTTCTTCTTATA 988 929 ATACCTGATTTGGGCTCTCAATTTTAACTGTAATGCTTCTTCTTCTTCTTCTTCTTCTTATA 988 614 ATACCTGATTTGGGCTCTCAATTTTAACTGTAATGCTTCTTCTTCTTCTTCTTCTTCTTATA 673 614 ATACCTGATTTGGGCTCTCAATTTTAACTGTAATGCTTCTTCTTCTTCTTCTTCTTCTTATA 673 989 GGTGAAAAGATTTGCTCTGCACTTTCAGTCTTTCGTTGCTTTCGTTGCTTTCGTTGCTT 1048 989 GGTGAAAAGATTTGCTCTGCACTTTCAGTCTTTCGTTGCTTTCGTTGCTTTCGTTGCTT 1048 674 GGTGAAAAGATTTGCTCTGCACTTTCAGTCTTTCGTTGCTTTCGTTGCTTTCGTTGCTT 733 674 GGTGAAAAGATTTGCTCTGCACTTTCAGTCTTTCGTTGCTTTCGTTGCTTTCGTTGCTT 733 1049 ATTGAAGAGATCATACCATCATCTTCCAAAGTCAATACCTCTTAATTTGGAGAGTATCTGGTA 1108 1049 ATTGAAGAGATCATACCATCATCTTCCAAAGTCAATACCTCTTAATTTGGAGAGTATCTGGTA 1108 734 ATTGAAGAGATCATACCATCATCTTCCAAAGTCAATACCTCTTAATTTGGAGAGTATCTGGTA 793 734 ATTGAAGAGATCATACCATCATCTTCCAAAGTCAATACCTCTTAATTTGGAGAGTATCTGGTA 793 1109 TTTTACCATGATTTTCTGACATGCTCAATATATGGAACCGTCTTCGCTATCAACATTCAT 1168 1109 TTTTACCATGATTTTCTGACATGCTCAATATATGGAACCGTCTTCGCTATCAACATTCAT 1168 794 TTTTACCATGATTTTCTGACATGCTCAATATATGGAACCGTCTTCGCTATCAACATTCAT 853 794 TTTTACCATGATTTTCTGACATGCTCAATATATGGAACCGTCTTCGCTATCAACATTCAT 853
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL MEDLINE PUBLISHED REFERENCE AUTHORS	Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giesi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pezole, G., Tonita, M., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2449) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216] cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/	BASE COUNT 626 a 558 g 578 G 687 C ORIGIN	Query Match 39.3%; Score 718.4; DB 11; Length 2449; Best Local Similarity 79.7%; Pred. No. 1.5e-129; Matches 875; Conservative 0; Mismatches 216; Indels 7; Gaps 2; 569 GCAGATGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 628 569 GCAGATGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 628 254 GGAGACGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATGACATGCGACTGTC 313 254 GGAGACGGAGCTTTTGAAGGACAGTACGAAAACAGTATCATCGGTACATG

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VERSION BO433768.1 GI:21172844
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1327 row: m column: 22
High quality sequence start: 83
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FEATURES

source

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Best Local Similarity 97.6%; Pred. No. 3.6e-108;
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Db 369 TTGGACTTATGATGGATCACAGGTTGATATAAATCTAGAGGACCAAGATGTAGACAAGAG 310
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RESULT 3

BM839817

LOCUS

DEFINITION

K-EST0116784 S13KMS5 Homo sapiens cDNA clone S13KMS5-32-E08 5',

mRNA sequence.

ACCESSION

BM839817

VERSION

BM839817.1 GI:19196226

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 655)

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: E column: 08
High quality sequence stop: 655.
Location/Qualifiers
1. 655

TITLE
JOURNAL
COMMENT

FEATURES
source

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/note="vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoR I which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
149 a 160 c 197 g 149 t

BASE COUNT 149 a 160 c 197 g 149 t
ORIGIN
Query Match 32.5%; Score 593.8; DB 12; Length 655;
Best Local Similarity 99.5%; Pred. No. 2.7e-105;
Matches 606; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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ACCESSION
BX332469 1 GI:30308099
VERSION
BX332469
KEYWORDS
EST.
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7788.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC012BG100P1
&cluster=7788.f. Contact : Feng Liang Email : fliang@lifetech.com
URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC012BG100P1.
FEATURES
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BASE COUNT 309 a 219 c 294 g 316 t 63 others
ORIGIN
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100%length, match=1392)
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MDVTFFDKQNSMKPFGSYDGTWDLILINENVDKDFDFNGSWELLINAKMGKN
RREGFYSYPPVTYSFVLRRLPLFYLLIPCLGLSFLVFLVFLPSDEGEKLSLSTS
VLVSLTVFLVDEIIPSSSKVPLIGELYLLFMIFVTLISIIIVTFVINVHRRSSSTY
HPNAPWVRLFLLEKLPRWLCMDKPRDRFSPDGTESKGTVRGKFPKPKKQTPDGER
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IFIPALKNWJHFRH"
polyA_signal
4569..4574
/notes="putative"
polyA_site
4589
/notes="putative"
BASE COUNT 1105 a 1106 c 977 g 1401 t
ORIGIN

Query Match 28.5%; Score 521.4; DB 11; Length 4589;
Best Local Similarity 64.5%; Pred. No. 3.3e-91;
Matches 839; Conservative 0; Mismatches 411; Indels 51; Gaps 2;

Qy 278 TCTATTCAAAACATGAAGATAGTTTCTTAAGATTTATTCAGACTACGAAAGATGG 337
Db 347 TCACTGGCTGAACATGAAGACGCACTCTCAGACATTTGTTCAGAGTTATCAGAAATGT 406
Qy 338 GTTCGCTCTGGGAACACCTGAATGACAAATAAAATAAAATTTGGACTTGCATATCT 397
Db 407 GTCCGCCCTGTGTGAATTCAGTGACATCAANAAGTGATTTTGGATTAAAGATATCT 466
Qy 398 CAATGTGTGATGGATGAGAAAATCAGTTAATGACAAACAAACGCTGTGTTGAAACAG 457
Db 467 CAGCTCTGATGTGGATGAAAGAAATCAGCTGATGACAAACAAACGCTGTGCTGAACAG 526
Qy 458 GAATGGATAGATGAAAATTAAGATGGAACCGCTGATGACATATGTTGGAATAAAAGTTATA 517
Db 527 GAATGGACAGACCAAAAATTTACGATGGAATCCCGAAGACTATGTTGGAATTAATTCGATA 586
Qy 518 CGTGTCTCTCAGACTCTGCTGACACACGACATCGTTTGTGTTGATGATGACAGATGGA 577
Db 587 AAGTTCCATCGGAGTCGCTGTGCTGCTGACATAGTCTCTTTTGAANAATGCTGACGGA 646
Qy 578 CGTTTGAAGGGAC---CAGTACGAAAACAGTCACTCAGGTACAAATGCGACTGTCAACCTGG 634
Db 647 CGTTTGAAGGCTCTCTCATGACCAAGGCCATTTGTAATCCAGCGAACCGTCAGTTGG 706
Qy 635 ACTCCACGGGCAACTACAAAGTTCCTGTACCAATAGATGTCAGTTTTCCTCCATTTGAC 694
Db 707 ACTCTCCCGCAGCTACAAAGTTCTCTGTACCAATGATGTACATTTTTCCTCCGCTTCGAT 766
Qy 695 CTTCAGAACTCTCCAGAAATTTGGTTCTTGGACTTATGATGATCAGAGTTTGATATA 754
Db 767 AAGCAGAACTGCTCAATGAAGTTCCGATCTCTGGACTTACGATGTTACATGGTCGACCTC 826
Qy 755 ATTCTAGAGGACCAAGATGTAGACAAGAGAGATTTTGTGATATGAGAGATGGAGATT 814
Db 827 ATTCTGATCAATGAACAGTTGACCGGAAAGACTTTTGTGATACGAGAGTGGAGATA 886
Qy 815 GTGAGTGAACAGGAGAGAAAGAAACAGAACCAAGCTGTCTGCTGGTATCCGATATGTC 874
Db 887 CTTAAATCAAAAGGGGATGAAGGGCAACAGAGAGAGAGGCTTTTACTCTCTATCCGCTTTGTT 946
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Qy 875 ACTTACTATTGTATCAAGCGCCTGCTCTCTTTTATACCTTGTCTCTTATAATACC 934
Db 947 ACCTACTCTTTTGTCTGAGAGCGCTGCCCTGTTTTACACCTCTCTTTTGTATAATACCC 1006
Qy 935 TGTATTGGGCTCTCATTTTAACTGATGCTTCTCTATCTTCTTCAATGAAGGTGA 994
Db 1007 TGCCTGGGCTGTCTTTTCTCAGGTCCTGGTGTCTTACCTACCTCCCGCAGGAAGGGAA 1066
Qy 995 AGATTGTGCTCTGCACACTTCACTGATGCTTCTTGAAGTGTCTTCTCTGTTGTTATGAA 1054
Db 1067 AAATCTCTCTTATCCACCTCGGTTTGGTTTCTTGAAGTGTCTTCTTGTATGAA 1126
Qy 1055 GAGATCATATACCATCATCTTTCAAAAGTCATACCTTAATTTGGAGAGTATCTGTTATTACC 1114
Db 1127 GAAATAATCCCGTCTTCTTCAAAAGTCATCCCTCTCATTTGGGAGTACCTCTCTTCAAT 1186
Qy 1115 ATGATTTTGTGACACTGTCAATATATGTAACCGTCTTCTGCTATCAACATTCATCATCGT 1174
Db 1187 ATGATATTTGTCAACGCTGTCTATATATGTCAGGTTTGTATTAATGTCCACACAGA 1246
Qy 1175 TCTTCTCTCAACATATCCATGCGCTTTGGTCCGCAAGATATTTCTTCAACGCTT 1234
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Qy 1235 CCCAAACTGCTTTGTCATGAGAAAGTCATGTAGACAGGTACTTCACTC----- 1280
Db 1307 CCGAGATGCTTTGTCATGAAGGACCCAGGACCGCTCTCTTTCCCGCATGGAACGGAG 1366
Qy 1281 -----AGAAAGAGAAACTGAGAGTGGTAGT 1306
Db 1367 AGTAAGGGAACCGTGGGGGGAATTTCCAGGGGAAAGAGAGAGAGTCTCTACAGTGAT 1426
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Db 1427 GGAGAAAGAGTCTCTGTCGCTTTCTTGGAGAGGCTCTGAGTCCATCAGATACATCTCG 1486
Qy 1367 AGACACATCATGAAGGAAATGATGTCGCTGAGGTTTGTCAAGATTGGAATTCATAGCC 1426
Db 1487 AGCATGTGAGAGGAAACATTCATCAGTCAGTTGTTTCAAGACTGGAATTCGTTGGCT 1546
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Db 1547 CAGGTTCTTGTACCGCATCTTCTCTGCTCTTCTGACAGCTTCGGTTTGGGCTCTGTC 1606
Qy 1487 GGCTTTTGTCTCTTATTTATAAATGSGCAATATATT 1527
Db 1607 CTGATTTTATTCAGCCTTGAAGATGTGGATACATCGTTT 1647
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RESULT 6
BU623054/c
LOCUS
DEFINITION
UI-H-FLJ-bgd-k-15-0-UI.s1 NCI-CCAP_FLI Homo sapiens cDNA clone
UI-H-FLJ-bgd-k-15-0-UI 3', mRNA sequence.
ACCESSION
BU623054
VERSION
BU623054.1 GI:23289269
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 701)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
```

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-46, AT-richLow_complexity
Seq primer: MI3 FORWARD
POLYA=Yes.

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10
11. Feature 11	Source 11
12. Feature 12	Source 12
13. Feature 13	Source 13
14. Feature 14	Source 14
15. Feature 15	Source 15
16. Feature 16	Source 16
17. Feature 17	Source 17
18. Feature 18	Source 18
19. Feature 19	Source 19
20. Feature 20	Source 20
21. Feature 21	Source 21
22. Feature 22	Source 22
23. Feature 23	Source 23
24. Feature 24	Source 24
25. Feature 25	Source 25
26. Feature 26	Source 26
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28. Feature 28	Source 28
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33. Feature 33	Source 33
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88. Feature 88	Source 88
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92. Feature 92	Source 92
93. Feature 93	Source 93
94. Feature 94	Source 94
95. Feature 95	Source 95
96. Feature 96	Source 96
97. Feature 97	Source 97
98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

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FEATURES             Location/Qualifiers
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     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="UI-H-FLI-bgd-k-15-0-UI"
     /tissue_type="Cell lines"
     /dev_stage="Adult"
     /lab_host="DH10B (Life Technologies)"
     /clone_lib="NCI CGAP FL1"
     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI_CGAP_FL1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGGTCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa."
     TAG_LIB="UI-H-FLI"
     TAG_TISSUE="Human Chondrosarcoma Grade 3 cell line mix"
     TAG_SEQ="GAGGTCGGTG"
239 a _122 c 102 g 238 t

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Query Match	27.6%	Score 505.4;	DB 13;	Length 701;
Best Local Similarity	99.8%;	Pred. No. 4.4e-88;		
Matches 506;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1322	AGAAACACATTTGAAAGCTGGCTCAATTCATTTGGCTACATTAACAAGACACATCATGAAG	1381	
DB	701	AGAAACACATTTGAAAGCTGGCTCGATTCATTTGGCTACATTAACAAGACACATCATGAAG	642	
QY	1382	GAAAAATGATCTCGTGCAGGTGTGTGAAGATTGGAAATTCATAGCCACGAGTCTTGTATCGG	1441	
DB	641	GAAAAATGATCTCGTGCAGGTGTGTGAAGATTGGAAATTCATAGCCACGAGTCTTGTATCGG	582	
QY	1442	ATGTTTCTGTGGACTTTTCTTTTCGTTTCAATTTGTTGGATCTCTGGGGCTTTTTGTTCTCT	1501	
DB	581	ATGTTTCTGTGGACTTTTCTTTTCGTTTCAATTTGTTGGATCTCTGGGGCTTTTTGTTCTCT	522	
QY	1502	GTTATTTATAATGGGCAATATATTAATAACAGTTTCATATTGGAAATCAAATAAGTGA	1561	
DB	521	GTTATTTATAATGGGCAATATATTAATAACAGTTTCATATTGGAAATCAAATAAGTGA	462	
QY	1562	AGCTCCCAAGGACTGAAGTATACATTTAGTTTAAACACACATATATCTGATGGCAGCTAT	1621	
DB	461	AGCTCCCAAGGACTGAAGTATACATTTAGTTTAAACACACATATATCTGATGGCAGCTAT	402	
QY	1622	AAAAATTATGAAAATGTAAGTTATGCTGTAATTTAGTGCAGAGCTTTAAACAGACTAAGTTG	1681	
DB	401	AAAAATTATGAAAATGTAAGTTATGCTGTAATTTAGTGCAGAGCTTTAAACAGACTAAGTTG	342	
QY	1682	CTAACCTCAATTTATGTTTAAACAGATGATCCATTTGAAACAGTTGGCTGTATGATCTGAAGTA	1741	
DB	341	CTAACCTCAATTTATGTTTAAACAGATGATCCATTTGAAACAGTTGGCTGTATGATCTGAAGTA	282	
QY	1742	ATAACTGTATGAGATACATTTGATCTTTGTAATAATAAGCAAAAATATTATCTGAACTGACTTA	1801	
DB	281	ATAACTGTATGAGATACATTTGATCTTTGTAATAATAAGCAAAAATATTATCTGAACTGACTTA	222	

Qy	1802	GTGAATAATCTAGTATTGTATCTCGG	1828
Db	221	GTGAATAATCTAGTATTGTATCTCGG	195
RESULT 7			
EX107344			
LOCUS	EX107344	Soares infant brain 1N1B Homo sapiens cDNA clone	linear mRNA 527 bp EST 06-FEB-2003
DEFINITION	IMAGE998K02266	IMAGE:43346, mRNA sequence.	
ACCESSION	EX107344		
VERSION	EX107344.1	GI:27834625	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 527)		
AUTHORS	Eberl, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radlof, U., Schneider, D. and Korn, B.		
TITLE	Human Unigeneset - RZPD3		
JOURNAL	Unpublished		
COMMENT	Contact: Ina Rolfes RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD: IMAGE998K02266. RZPDLIB: I.M.A.G.E.B. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response=libNo972 Contact: Ina Rolfes RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; Contact RZPD (clone@rzpd.de) for further information. Seq primer: M13u, Primer sequence: CGTTGTAACGACGCCAGT.		
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source	1..527		
Location/Qualifiers			

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1. 527
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/db_xref="taxon:9606"
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/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AACTGGAAGATTCGGCCGGCAGGAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Donaldo."
138 a 117 c 99 g 173 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 97.6%; Score 505; DB 13; Length 527;
Matches 527; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 809 GAGATTGTGAGTGCAACGAGGAGCAAGAGAAACAGAACCGACAGCTGTGCTGGTATCCG 868
1 GAGATTGTGAGTGC -ACAGGAGCAAGAGAAACAGAACCGACAGCTGTGCTGGTATCCG 59

869 TATGTCATTACTCAATTTGTAATCAAGCGCTGCCTCTCTTTTATACCTGTGCTCTATA 928
60 TATGTCATTACTCAATTTGTAATC -AGGCGCTGCCTCTCTTTTATACCTGTGCTCTATA 118

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FEATURES
source
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/organism="Gallus gallus"
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/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="Chesf589f19"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSQCHN55"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
BASE COUNT      208 a 141 c 138 g 257 t
ORIGIN
Query Match      27.0%; Score 493.6; DB 13; Length 744;
Best Local Similarity 81.4%; Pred. No. 8.7e-86;
Matches 596; Conservative 0; Mismatches 134; Indels 2; Gaps 2;
QY 562 TGATATGAGATGAGCGTTTGAAGGGACCACTAGTACGAAACAGTCATCAGTACAAATGG 621
Db 1 TGACATGAGATGAGCGTTTGAAGGGACCGTCTACTAAACTGTGTAATAATATGATGG 60
QY 622 CACTGTACCTGAGCTCCACCGGAAACTACAAAAGTTCCTGTACATAGATGTCAGTT 681
Db 61 CACCATTGCTGGACTCCACCAAGCAAAATATATAAAGTTCCTGTACTATTGACGTAACCTT 120
QY 682 TTTCCTATTTGACCTTCAGACTGTTCCATGAATTTGGTCTTCCTGGACTTATGATGATC 741
Db 121 CTTTCCCTTTGACCTCCAAACTGCTATGAATTTGGTCTTCCTGGACTTATGATGATC 180
QY 742 ACAGGTTGATATAATTTAGAGGACCAAGATAGTACAAAGAGAGATTTTGTATAATGG 801
Db 181 CCAGGTTGATATAATTTAGAGATATGATGTTGACAAAGAGACTTTTGTATAATGG 240
QY 802 AGAATGGAGATTTGAGTGCAACAGGGAGCAAGAAACAGAACCGACAGCTGTGTCTG 861
Db 241 AGAATGGGAAATAGTGACTGCAACAGGGAGCAAGGAAATAGAACTGATGATGCTGCTG 300
QY 862 GTATCCGTATGCTACTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGT 921
Db 301 GTATCCCTTTGTATCATATTTATTAATTAATAGACGTTTACCACCTTTTATACAGCTGT 360
QY 922 CTTTATAATACCTGTATTTGGCTCTCATTTTAACTGACTGTGCTTCTATCTTCCTTC 981
Db 361 TCTCATCATCTCTGTATTTGACTTCTTTCTTAAGTCTGCTGCTCTCTATCTTCCTTC 420
QY 982 AAATGAAGTGAAAGATTTGCTCTGCACCTTCAGTACTGTGTGCTTTGACTGTCTTCT 1041
Db 421 AAATGAAGTGAAAGATTTTCCCT-TTAACTTCAGTCTGCTGTATCTCTGACTGTTTCT 479
QY 1042 TCTGTTATTGAGAGATCATACCATCATCTTCAAAAGTCATACCTCTAAATGGAGATA 1101
Db 480 TCTTGAATTTGAAGAGATTAATTCATCGTCTTTCTAAAGTTATCCCACTTATAGAGAATA 539
QY 1102 TCTGTTATTACCATGATTTTGTGACACTGTCAATTATGTAACCGTCTTCGCTATCAA 1161
Db 540 CTTGGTGTTTACTATGATTTTGTGACATTTGTCATTGTGATTAACCTGCTTTGCTATCAA 599
QY 1162 CATTTCATCATGTTCTTCTCTCAACATAATGCCATGGCGCTT-TGGTCCGCAAGATAT 1220

Db 600 TATTCATCACCGTTTCTTCATCTACACAATGCCATGCCACCTTGGGGTTCGCAAGATAT 659
QY 1221 TTCTTCACACGTTCCCAAACTGCTTTTCATGAGAGAGTCATGTACAGAGTACTTCACTC 1280
Db 660 TTCTTCACAAACTTCCCAAGCTGCTGTGATGAGAGATCATGTAGATAGTACTTTGCTC 719
QY 1281 AGAAGAGAGGAAA 1292
Db 720 AGAAGAGGAGAAA 731

RESULT 10
LOCUS AV748726 538 bp mRNA linear EST 19-OCT-2000
DEFINITION AV748726 NPC Homo sapiens cDNA clone NPCAAC09 5', mRNA sequence.
ACCESSION AV748726
VERSION AV748726.1 GI:10906574
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 538)
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel.: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mshions.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
LOCATION/Qualifiers
1. .538
/organism="Homo sapiens"
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/clone="NPCAAC09"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="NPC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      122 a 122 c 155 g 131 t 8 others
ORIGIN
Query Match      26.5%; Score 485.2; DB 9; Length 538;
Best Local Similarity 96.7%; Pred. No. 3.8e-84;
Matches 525; Conservative 0; Mismatches 10; Indels 8; Gaps 3;
QY 49 CGTTTGTCTCACACTCAGTCTGCTGCTATTCCTCCCAAGAGTTCGCTTCCCGCGC 108
Db 1 CGTTTGTCTCACACTCAGTCTGCTGCTATTCCTCCCAAGAGTTCGCTTCCCGCGC 60
QY 109 GCGCGTCGAGAGCGGCTGCCCGGTCGCCGCGGGCGGGCGATGGCGGCGGGG 168
Db 61 GCGCGTCGAGAGCGGCTGCCCGGTCGCCGCGGGCGGGCGATGGCGGCGGGG 120
QY 169 GTGAGGCGCGCGCGCTCGCGCTGCTCTTCTGCTCAGCTGTGTGCGGGCGCTGCGG 228
Db 121 GTGAGGCGCGCGCGCTCGCGCTGCTCTTCTGCTCAGCTGTGTGCGGGCGCTGCGG 180
QY 229 TCTAGCGGCGCGCGCGCGCGCGCGCGCGCGAGAGGATTTCTGAACCTTCTTCTATTGCAAA 288
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High quality sequence stop: 493.
FEATURES
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      /lab_host="DH10B (T1 phage-resistant)"
      /clone_lib="NIH MOC 58"
      /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
      SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc);
      Double-stranded cDNA was prepared from cell line RNA.
      and 3' adaptors were used in cloning as follows: 5'
      adaptor sequence: 5'-CACGGCATATGGCC-3' and 3' adaptor
      sequence: 5'-ATTCTAGAGCGGCGGCCACATG-dT(30)BN-3'
      (where B = A, C, or G and N = A, C, G, or T). Average
      insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
      contained inserts by PCR. This library was constructed for
      full-length clones and was constructed by Clontech
      Laboratories (Palo Alto, CA)."
  BASE COUNT      201 a 142 c 180 g 232 t
  ORIGIN
    Query Match      25.6%; Score 467.4; DB 10; Length 755;
    Best Local Similarity 93.4%; Pred. No. 1.le-80;
    Mismatches 565; Conservative 0; Mismatches 31; Indels 9; Gaps 7;
  QY 686 CCAATTGACCTTCAGAACCTGTTCCATGAATTTGGTCTTGACCTATGATGATCAG 745
  Db 1 CCAATTGACCTTCAGAACCTGTTCCATGAATTTGGTCTTGACCTATGATGATGATCAG 60
  QY 746 GTTGATATAATTTCTAGAGACCAAGATGTAGACAGAGAGATTTTTTGTATAATGGAGAA 805
  Db 61 GTTGATATAATTTCTAGAGACCAAGATGTAGACAGAGAGATTTTTTGTATAATGGAGAA 120
  QY 806 TGGGAGATTGAGTGCACACGGGAGCAAGAAAGAAACAGAACCGACGTGTGCTGTAT 865
  Db 121 TGGGAGA-TGTGAGTGCAACAGGGAGCAAGAAAGAAACAGAACCGACGTGTGCTGTAT 179
  QY 866 CCGTATGTCACCTACTATCTTATCAAGCGCTGCTCTTTTATACCTTGTCTCTT 925
  Db 180 CCGTATGTCACCTACTATCTTATCAAGCGCTGCTCTTTTATACCTTGTCTCTT 239
  QY 926 ATAATACCTGTATTTGGGCTCTCAATTTTAACTGTACTTGTCTTCTATCTTCAAT 985
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LOCUS AV749460 NPC Homo sapiens cDNA clone NPCAAG11 5', mRNA sequence.
DEFINITION AV749460
ACCESSION AV749460
VERSION AV749460.1 GI:10907308
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 542)
Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbshiem@stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
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Db      418 ANATGGAACCTGATGACTATGTTGGAAAT--NGTTATACGTGTTCTTCAGACTCTGNN 474
QY      539 TGGACACACGACATCGTTTTTGTGTAATGCGAGATGGACGTTTGAAGG 588
Db      475 TGGACACACGACATCGTTTTTGTGTAATGCGAGATGGACGCGTTTGGGG 524

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LOCUS   BQ225664
DEFINITION ACENCOURT 7593049 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070546
5' mRNA sequence.
ACCESSION BQ225664
VERSION   BQ225664.1 GI:20407064
SOURCE    EST.
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 858)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-rc@mail.nih.gov
          Tissue Procurement: DCTD/DTF/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13355 row: a column: 11
          High quality sequence stop: 472.

FEATURES             source
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     /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
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BASE COUNT 281 a 149 c 158 g 270 t
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Query Match      24.2%; Score 442.4; DB 13; Length 858;
Best Local Similarity 99.8%; Pred. No. 8.1e-76;
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1445 TTCTCTGGGACTTCTTTTCGTTTCATATGTTGGATCTCTTGGGCTTTTGTCTCTGTT 1504
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QY      1505 ATTTATAAATGGGCAATATATTAAATACCAAGTTTCATATTCGAATGCAATAAGTGAAGC 1564
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QY      1565 CTCCCAGGACCTGAAGTATACATTTAGTTTAAACACATATATCTGATGGCACCTATAAA 1624
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QY      1625 ATTATGAAAATGTAAGTTATGTTTAAATTTAGTGCAGAGCTTTAAACAGACTAAGTTGCTA 1684
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QY      1685 ACCTCAATTTATGTTTAAACAGATGATCCATTTGAACAGTTGGCTGTATGACTGAAGTAATA 1744
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QY      1745 ACTGATGAGATACATTTGATCTGTGTAATAATAGCAAAATATTATCTGAACTGGACTAGTG 1804
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QY      1805 AAAAAATCTAGTATTGTTATCTCTGG 1828
Db      421 AAAAAATCTAGTATTGTTATCTCTGG 444

RESULT 15
LOCUS   AK017571
DEFINITION Mus musculus 8 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:5730417K16 product:NEURONAL ACETYLCHOLINE
RECEPTOR PROTEIN, BETA-3 CHAIN PRECURSOR homolog [Rattus
norvegicus], full insert sequence.
ACCESSION AK017571
VERSION   AK017571.1 GI:12856874
KEYWORDS  HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
AUTHORS   High-efficiency full-length cDNA cloning
TITLE     Meth. Enzymol. 303, 19-44 (1999)
JOURNAL   99279253
MEDLINE   PUBMED
PUBMED    10349636

REFERENCE 2
AUTHORS   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   PUBMED
PUBMED    11042159

REFERENCE 3
AUTHORS   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE     RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   PUBMED
PUBMED    20530913

REFERENCE 4
AUTHORS   Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
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Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:45:16 ; Search time 1739 Seconds
(without alignments)
3502.742 Million cell updates/sec

Title: US-09-703-951A-7

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	324.8	17.8	2068	10	US-10-349-836-1
5	315.6	17.3	1908	13	Sequence 1, Appli
6	315.6	17.3	1908	13	Sequence 3, Appli
7	315.6	17.3	2015	15	US-10-175-523-52
8	314.8	17.2	1743	13	Sequence 52, Appl
9	314	17.2	1584	15	Sequence 297, App
10	308.8	16.9	1756	10	US-10-349-836-9
11	303.2	16.6	3496	13	Sequence 91, Appl
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14	295	16.1	296	15	Sequence 5, Appli
15	294.4	16.1	1667	15	Sequence 1659, Ap
					Sequence 1659, Ap
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					Sequence 27, Appl

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280.8 15.4 1869 10 US-09-941-179A-10
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260 14.2 1869 10 US-09-941-179A-2
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ALIGNMENTS

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; APPLICANT: Elliott, Kathryn J.
; Harbold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

Db 1801 AGTGAATACTAGTATTGTATCTCTGG 1828

RESULT 2
US-10-349-836-15
; Sequence 15, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; NAME/KEY: 5'UTR
; LOCATION: 98...1474
; OTHER INFORMATION: beta3 human neuronal nicotinic
; acetylcholine receptor
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Db 227 GTCCGCCCTGTATTACATTCTAATGACACCAATAAAGTATATTTGGATTGAAATATCC 286

398 CAATTGGTGGATGTGGATGAGAAAATCAGTTAATGACAAACAGCTCTGGTTGAAACAG 457
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458 GAATGGATAGATGTAATAATTAAAGATGGAACCTGATGACTATGGTGGGATAAAGTTATA 517
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518 CGTGTTCCTTCAGACTCTGTCTGGACACCAAGATCATCGTTTGTGTAATGATGATGGA 577
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1127 CAAATTTACTTTGATGAAAGATCATGTGATGCTACTCATCCCCAGAGAGAGAG 1186
1275 -----TCACTCAGAAAGAGAACTGAGAGTGGTAGT 1306
1187 AGTCAACCCAGTAGTCAAGGCAAGTCTCGAAAAAAGAAACAGAAACAGCTTAGTAT 1246
1307 GGACCAAAATCTCTAGAAAACATTTGGAAGCTGGCTCAATTTCTATTTCGCTTACATTACA 1366
1247 GGAGAAAAAAGTCTAGTTGCTTTTTTGGAAAAAGCTGCTGATTCATTTAGATACATTTCC 1306
1367 AGACACATCATGAGGAAAAATGATGCTGAGGTTGTTGAGATTTGGAATTCATAGCC 1426
1307 AGACATGGAAGAAAGAACATTTTATCAGCAGGTAGTACAAAGCTGGAATTTGTAGCT 1366
1427 CAGGTTCTTGATCGATGTTTCTGTTGACTTTTCTTTTCTGTTTCAATTTGTTGGATCTCTT 1486

Db 1367 CAAGTCTTACCGCAATCTTCCTGTGGCTCTTTCTGATAGTGTACAGTAAACAGGCTCGGTT 1426
Qy 1487 GGGCTTTTGTCTGCTGTTATTTATAAATGGGCAATATATAATACAGGTTTCATATTGGA 1546
Db 1427 CTGATTTTACCCCTGCTTGAAGATGTGGCTACATAGTTACCATAGGAATTTAAAGA 1486
Qy 1547 AATGCAATAAGTGAACCCCTCCCAAGGAC 1576
Db 1487 CATAAGACTAAATTACACCTTAGACCTGAC 1516

RESULT 3

US-10-349-836-1
; Sequence 1, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 555...2141
; OTHER INFORMATION: alpha2 subunit of human neuronal
; nicotinic acetylcholine receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-349-836-1

Query Match 18.3%; Score 334.6; DB 13; Length 2664;
Best Local Similarity 61.3%; Pred. No. 1.8e-79;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;

RESULT 4
US-09-892-985-1
; Sequence 1, Application US/09892985

Qy 292 TGAAGATAGTTGCTTTAAGGATTTATTTCAAGACTACGAAAGATGGGTTGCTCTGTGGA 351
Db 728 TGAGGACCGGCTCTTCAAACACACCTTTCGGGGCTACAACCGCTGGCGCGCCGGTGCC 787
Qy 352 ACACCTGAATGACAAAATAAAATAAAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db 788 CAACACTTCAGACGCTGGTGATTTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 847
Qy 412 GGATGAGAAAAATCAGTTAATGACAAACAAACGCTCTGGTTGAAACAGGAATGGATAGATGT 471
Db 848 GGATGAGAGAACCAAAATGATGACCAACCAACGCTCTGGCTAAAACAGAGATGGAGCGACTA 907
Qy 472 AAAATTAAGATGGAACCTCGATGACTATGCTGGAATAAAAGTTTATACGTGTTCTCTTCAGA 531
Db 908 CAAACTGGCTGGAAACCCCGCTGATTTTGGCAACATACATCTCTCAGGGTCCCTCTCTGA 967
Qy 532 CTCTGTCTGGACACAGACATCGTTTGTGTTGTTGTAATGACAGATGGAGGTTTGAAGGAC 591
Db 968 GATGATCTGGATCCCGACATTTGTTCTTACAACAATGCAGATGGGGAGTTTGCAGTGAC 1027
Qy 592 ---CACTAGCAAAACAGTCAATGAGTACAGTGCACCTGTCCACCTGCAGCTCCACGGCAAA 648
Db 1028 CACATGACCAAGGCCCACTCTTCCACGGGCACTGTGCACTGGTGCCCGGCCAT 1087
Qy 649 CTACAAAAGTTCTGTACCATAGATGTACAGTTTTTCCCATTTTGACCTTTCAGAACTGTTTC 708
Db 1088 CTACAAAGAGCTCTGCAGCATCGACGTCACTTCTTCCCTTCGACCAAGCAAACTGCAA 1147
Qy 709 CATGAAATTTGGTTCTTGGACTTATGATGATGATCAGGTTGATATTAATTTAGAGNCCA 768
Db 1148 GATGAAGTTTGGCTCTCTGGACTTTATGACAAAGGCAAGATCGACCTGGAGCAGATGGAGCA 1207
Qy 769 AGATGTAGACAAGAGAGATTTTTTTCATAATGAGAGATGGAGATGTGAGTCAACAGG 828
Db 1208 GACTGTGGACCTGAAGGACTACTGGAGAGCGGAGTGGGCCATCGTCAATGCCACGGG 1267
Qy 829 GAGCAAGGAAACAGAACCGACAGCTGTGTTC-----TGGTATCCGTATGTCTACTTACTC 882
Db 1268 CACCTACACAGCAAGAAGTACGACTGTCTGGCGGAGATCTACCCCGAGCTCACTAGCG 1327
Qy 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATTAATACCTTGTATTGG 942
Db 1328 CTTCTGTCATCCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATCTCCCTGCTGCT 1387
Qy 943 GCTCTCATTTTAACTGTACTTGTCTTCTTCAATGAAGGTGAAAGATTTG 1002
Db 1388 CATCTCTGCTCACTGTGTGTCTTCTACCTGCGCCCTCGAGCTGCGGCGAGAGATCAC 1447
Qy 1003 TCTCTGCACTTCAGTACTTGTGTCTTGTGACTGTCTTCTTCTTCTTGTATTGAAGAGATCAT 1062
Db 1448 GCTGTGCATTTGGTGTCTGTCTCACTCACCGTCTTCTGCTGCTCATCACTGAGATCAT 1507
Qy 1063 ACCATCATTTTCAAAAGTCATACCTCTAATTGAGAGATGCTGGTATTATACCATGATTTT 1122
Db 1508 CCGTCCACCTCGCTGCTCATCCCGCTCATCCGCTCATCGGAGTACCTGCTGTTTACCATGATCTT 1567
Qy 1123 TGTGACACTGTCAATTTATGTAACCGCTTGTGCTATCAATTCATCATCGTCTTCTTCTC 1182
Db 1568 CGTCACCTGTCCATCGTCACTACCGCTTCTGCTCAATGTGCAACACCGCTCCCGCAG 1627
Qy 1183 AACACATAATGCCATGGCGCTTGTGTCGCAAGATATTTCTTCAACAGCTTCCCAAACT 1242
Db 1628 CACCCACA---CAATGCCCACTGGGTGGGGGGGCGCTTCTGGGCTGTGTGCGCGGTG 1684
Qy 1243 GCTTTCATGA 1253
Db 1685 GCTTCTGATGA 1695

Patent No. US20020111463A1
 GENERAL INFORMATION:
 APPLICANT: Elliott, Kathryn J.
 Ellis, Steven B.
 Harpold, Michael M.
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heller Ehrman White & McAuliffe
 STREET: 4250 Executive Square, 7th Floor
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/892,985
 FILING DATE: 27-Jun-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/466,589,
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9949B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-450-8400
 TELEFAX: 619-587-5360
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2068 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 166..1752
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-892-985-1

Query Match 17.8%; Score 324.8; DB 10; Length 2068;
 Best Local Similarity 59.9%; Pred. No. 7e-77;
 Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;
 292 TGAAGATAGTTGGCTTAAGGATTTATTTCAAGACTACGAAAGATGGGTTGCTCGTGTGGA 351
 339 TGAGACCGGCTTTCACACACCTTTCCGGGGCTTACACCGCTGGGCGCGCCGGTCCC 398
 352 ACACCTGAATGACAAATAAATAAATTTGGACTTGCATATATCTCAATTTGGTGGATGT 411
 399 CAACACTTCAGACGGTGGTGGTGGCTTTGGACTGTCCATCGCTCAGCTCATCATGT 458
 412 GGATGAGAAATAGTATGACACAAACCTCTGGTTGAAACAGGAATGATAGATGT 471
 459 GGATGAGAAACCAATATGATGACCAACCAACCTCTGGCTTAAACAGGAGTGGAGCGACTA 518
 472 AAAATTAAGATGGAACCCCTGATGACTATGTGGTGAATAAAGTTATACGTGTTCTTCA 531
 519 CAAACTGGCTGGAACCCCGCTGATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578

532 CTCCTCTGGACACGACATCGTTTCTTTGTAATGAGATGACGTTTGAAGGGAC 591
 579 GATGATCTGGATCCCGACATTTCTCTCAACAACAAANNNTGGGAGTTTGCAGTACCCCA 638
 592 CAGTACGAAACAGTCATCAGTACAATGGCACTGTCACTGAGCTCCACCGGCAACTA 651
 639 CATGACCAAGGCCACCTCTTCTCACGGGCACTGTGCACTGGGTGCCCCCGCCATCTTA 698
 652 CAAAAGTTCTGTACATAGATGTCAACGTTTTTCCCATTTGACCTTTCAGAACTGTTCCAT 711
 699 CAAGAGCTCTTCAGCATCGACGTCACCTTCTTCCCTTCGACCAAGCAACTGCAAGAT 758
 712 GAAATTTGGTCTTGGACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
 759 GAAATTTGGTCTTGGACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
 772 TGTACACAAGAGAGATTTTGTGATAATGGAGAAATGGGAGATTTGAGTGAACAGGGAG 831
 819 TGTGACCTGAGGACTACTGGGAGAGCGGAGATGAGGAGGATCTACCCGAGCTCACCCTAG 878
 832 CAAAGGAAACAGAACCCGACAGCTGTTGC-----TGGTATCCGTATGTCACCTTACTCAT 885
 879 CTACAAACAGCAAGATGACGACTGCTGCGCGGAGATCTACCCGAGCTCACCCTAGCCCTT 938
 886 TGTATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATATACCTGATGATGAGGCT 945
 939 CGTCATCCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCTCAT 998
 946 CTCATTTTAACTGACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1005
 999 CTCCTGCTCACTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1058
 1006 CTGCACTTCACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1065
 1059 GTGATTTGGTGTGCTGCTCACTCACCGTCTTCTGCTGCTCATCATGATGATCATCCC 1118
 1066 ATCATTTCAAAAGTCATACCTCTAAATGGAGAGATATCTGATTTTACCATGATTTTGT 1125
 1119 GTCCACCTCGCTGCTCATCCGCTCATCGGAGATACCTGCTGTTTCCACCATGATCTTGT 1178
 1126 GACACTGTCAATATGTAACGCTTTCGCTATCAACATTCATCATCTTCTTCTTCTTCT 1185
 1179 CACCTGTCCATCGTCATCACCGTCTTCTGCTCTCAATGTGAGACCAACCGCTCCCCAG 1238
 1186 ACATAATGCCATGCGCTTGTGCTCGCAAGATATTTCTTCAACGCTTCCCAAACTGCT 1245
 1239 CCACA---CCATGCCCACTGGGTGCGGGGGGGGCTTCTGCGGCTGTGTGCGCGGCT 1295
 1246 TTGCATGA 1253
 1296 TCTGATGA 1303

RESULT 5

US-10-349-836-3
 ; Sequence 3, Application US/10349836
 ; Publication No. US20030138911A1
 ; GENERAL INFORMATION:

APPLICANT: Elliott, Kathryn J.
 Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

Query Match		17.3%;	Score 315.6;	DB 15;	Length 1908;
Best Local Similarity		59.8%;	Pred. No. 2.1e-74;		
Matches 588;		Conservative 0;	Mismatches 384;	Indels 12;	Gaps 3;
QY	285	CAAAACATGAAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAAGATGGGTTCGTC	344		
DB	281	CAGAGCTGAGCAGCGTCTATTGAGCGGCTGTTTGAAGATTAACAATGAGATCATCCGGC	340		
QY	345	CTGTGGAAACACCTGAATGACAAATAAAATTTTGGACTTGCATATATCTCAATGG	404		
DB	341	CTGTAGCAACGTGTCTGACCCAGTCATCATCTTCAGGTGTCCATGCTCTAGCTGG	400		
QY	405	TGATGTGTGATGAGAAAATCAGTTAATGACAAACAGCTCTGGTTGAAACAGGAATGA	464		
DB	401	TGAAGGTGATGAAGTAAACCAAGATCATGGAGCAACCTGTGGCTCAAGCAAATCTGA	460		
QY	465	TAGATGTAATAATTAAGATGGAACCTGTGACTATGTTGGATGAATAAAGTTATACGTGTC	524		
DB	461	ATGACTACAAGCTGAAGTGGAAACCCCTCTGACTATGTTGGGGCAGATTCATGCGTGCC	520		
QY	525	CTTCAGACTCTGTCTGGACACAGACATCGTTTGTGTTGATTAATGAGATGGACGTTTGT	584		
DB	521	CTGCACAGAGATCTGGAGCCAGACATTTGCTGTATATAACATGCTGTGGGATTTCC	580		
QY	585	AAGGG---ACCAGTACGAAAACAGTCAATCAGGTACAATGGCACTGTCACTGGACTCCAC	641		
DB	581	AGGTGGACGACAAAGCAACCAAGCTTACTCAAGTACACTGGGAGGTGACTTGGATACCTC	640		
QY	642	CGGCAAACTACAAAGTTCTGTACCATAGATGTCAAGTTTTCCTCATTTGACCTTCAGA	701		
DB	641	CGGCACTCTTTAAGAGCTCTGTAAATTCGACGTGACCTACTTCCCGTTTGTATTACCAA	700		
QY	702	ACTGTTTCATGAAATTTGGTCTTGGACTTATGATGATCAAGTCTGATATAATTTCTAG	761		
DB	701	ACTGTACCATGAGTTGGTTCTGCTCTAGATAAGCGGAAATCGATCTGTCCTGA	760		
QY	762	AGGACCAAGATGTAGCAAGAGAGATTTTGTGATAATGGAAATGGGAGATTTGAGTG	821		
DB	761	TGGCTCTTCCATGAACCTCAAGGACTATTGGGAGAGCGGAGTGGGCCATCATCAAG	820		
QY	822	CAACAGGAGGCAAGGAAACAGACCGACAGCTGTGTCTGG-----TATCGTATGTCA	875		
DB	821	CCCCAGGCTACAAACACGACATCAAGTACAACTGCTGGAGGAGATCTACCCCGACATCA	880		
QY	876	CTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATAATACCT	935		
DB	881	CATCTCGCTGATACATCGGCGCTGCTGCTTCTTACACCATCAACCTCATCATCCCT	940		
QY	936	GTATTGGCTCTCATTTTAACTGTAATTGTTCTCTATCTTCTTCAAAATGAAGTGAAA	995		
DB	941	GCTGCTCATCTCTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1000		
QY	996	AGATTGTCTGCACTTCAGTACTGTGTGCTTGTGACTGTCTCTCTCTCTCTCTCTCTCT	1055		
DB	1001	AGGTGACCTGTGCAATTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1060		
QY	1056	AGATCATACCATCATCTTCAAAAGTCATACCTCTAAATTTGGAGAGTATCTGTTATTACCA	1115		
DB	1061	AGACCATCTCTCACTCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1120		
QY	1116	TGATTTTGTGACACTGTCAATTAATGTAACCGTCTCTGCTATCAACATTTTCATCTGTT	1175		
DB	1121	TGATTTTGTAACTTGTCT	1180		
QY	1176	CTTCTCTCAACATTAATGCAATGGCGCTTTGGTCCGCAAGATATTTCTTCAACGCTTC	1235		
DB	1181	CCCCAGAC	1237		
QY	1236	CCAAACTGCTTTGATGAGAGTC	1259		
DB	1238	CCAGGTCATGTTTATGACCGGC	1261		

RESULT 7
US-10-084-817-297
; Sequence 297, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 297
; LENGTH: 2015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1292280CB1
US-10-084-817-297

Query Match		17.3%;	Score 315.6;	DB 15;	Length 2015;
Best Local Similarity		59.8%;	Pred. No. 2.1e-74;		
Matches 588;		Conservative 0;	Mismatches 384;	Indels 12;	Gaps 3;
QY	285	CAAAACATGAAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAAGATGGGTTCGTC	344		
DB	215	CAGAGCTGAGCAGCGTCTATTTCAGCGGCTGTTTGAAGATTAACAATGAGATCATCCGGC	274		
QY	345	CTGTGGAAACACCTGAATGACAAATAAAATTTTGGACTTGCATATATCTCAATGG	404		
DB	275	CTGTAGCAACGTGTCTGACCCAGTCATCTCCATTTTCGAGGTGTCCATGCTCTCAGCTGG	334		
QY	405	TGATGTGAGTGAAGAAATTCAGTTAATGACAAACAGCTCTGGTTGAACAGGAATGA	464		
DB	335	TGAAGGTGGATGAAGTAAACAGATCATGGAGCAACCTGTGGCTCAAGCAAAATCTGGA	394		
QY	465	TAGATGTAATAATTAAGATGGAACCCCTGATGACTATGTGGAATAAAAGTTATACGTGTC	524		
DB	395	ATGACTACAGCTGAAGTGGNACCCCTCTGACTATGTGGGCGAGAGTTCTGCTGTCTCC	454		
QY	525	CTTCAGACTCTGTCTGGACACAGACATCGTTTGTGTTGTAATAATGCAAGATGGACGTTTG	584		
DB	455	CTGCACAGAAAGATCTGGAAGCCAGACATTTGCTGTATATAACAATGCTGTGGGATTTCC	514		
QY	585	AAGGG---ACCAGTACGAAAACAGTCATCAGTTACATGGCACTGTCACTGGACTCCAC	641		
DB	515	AGGTGGACGCAAGCAACCAAGCCCTTACTCAAGTACACTGGGGAGGTGACTTGGATACCTC	574		
QY	642	CGGCAAACTACAAAGTTCTGTACCATAGATGTACGTTTTCCTCATTTGACCTTCAGA	701		
DB	575	CGGCCATCTTTAGAGCTCTCTGTAATAATCGACGTGACTTACTTCCGTTTGTATTACCAA	634		
QY	702	ACTGTTCCATGAAATTTGGTCTTGTGACTTATGATGGATCACAGGTTGATATAATCTAG	761		
DB	635	ACTGTACCATGAAGTTCGGTTCCTGCTCTACGATAGGCGGAAATCGATCTGGTCTCTGA	694		
QY	762	AGGACCAAGATGTAGACAAAGAGATTTTGTGATAATGAGATGGAGATTTGTAGTG	821		
DB	695	TCGGCTCTTCCATGAACCTCAAGGACTATTGGGAGAGCGGCGAGTGGGCCATCATCAAAG	754		
QY	822	CAACAGGAGCAAGGAAACAGAACCCAGACGCTGTGTCTCTG-----TATCCGTTATGTCA	875		
DB	755	CCCCAGGCTACAAACACGACATCAAGTACAACTGCTGCGAGGAGATCTACCCGACATCA	814		
QY	876	CTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATAATACCT	935		

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-892-985-3

Query Match 16.9%; Score 308.8; DB 10; Length 1756;
Best Local Similarity 59.2%; Pred. No. 1.4e-72;
Matches 583; Conservative 1; Mismatches 388; Indels 12; Gaps 3;

QY 285 CAAAACATGAAGTAGTTTCCTTAAGGATTATTCAGACTACGAAAGATGGTTTCGTC 344
DB 130 CAGAGGCTGAGCACCGCTCTATTGAGCGCTGTTTGAAGATTACATGAGATCATCGGC 189
QY 345 CTGTGGAACACCTGAATGACAAAATAAAATTAATTTGACTTGCAATATCTCAATTGG 404
DB 190 CTGTGGCAACGCTGTGACCCAGTCATCATTCATTCGAGGTGTCATCTCAGCTGG 249
QY 405 TGGATGTGGATGAGAAAATCAGTTAATGACAAACAACTGCTGGTTGAAAACAGGAATGGA 464
DB 250 TGAAGGTGGATGAAGTAAACAGATCATGAGACCAACCTGTGGCTCAAGCAAAATCTGM 309
QY 465 TAGATGTAATTAAGATGAAACCTGATGACTATGCTGGAATAAAGATTATAGGTTC 524
DB 310 ATGACTACNAGCTGAAGTGAACCCCTCTGACTATGTTGGGCGAGAGTTATCGGTGTC 369
QY 525 CTTCAGACTCTGCTGACACACGACATCGTTTGTGTTGTAATGACAGATGGAGTTTG 584
DB 370 CTGCACAGAGATCTGAGGACGACATTTGCTGTATACATGCTGTGGGATTTCC 429
QY 585 AAGGG---ACCAGTACGAAACAGTCAATGAGTCAATGACCTGTGACCTGGACTCCAC 641
DB 430 AGGTGGACGACAAACAGCCCTTACTCAAGTACACTGGGAGGTGACTTGGATACCTC 489
QY 642 CGGCAACTACAAAGTTCCTGTACATAGATGCTGTTTCCCAATTTGACCTTCAGA 701
DB 490 CGGCCATCTTTAAGAGCTCCTGTAATAATCGACGTGACCTACTTCCCGTTTGTATACCAA 549
QY 702 ACTGTTCCATGAATTTGGTTCTTGGACTTATGATGATCAGGTTTGATATAATCTAG 761
DB 550 ACTGTACATGAGTTCCGGTTCCTGCTCCTACGTAAGGGAATGACGCTGCTCTGA 609
QY 762 AGGACCAAGATGTAGACAGAGAGATTTTGTGATAATGAGAAATGGGAGATTGTGAGTG 821
DB 610 TCGSCTCTTCCATGAACCTCAAGSACTATTGGGAGAGCGGAGTGGGCCATCAAG 669
QY 822 CAACAGGAGCAAGGAAACAGAACCGACAGCTGTTGCTGG-----TATCCGTATGCA 875
DB 670 CCCAGGYTATAACACGACATCAAGTACAACTGCTCGAGGAGATCTACCCGACATCA 729
QY 876 CTTACTCTATTGTAATCAAGCGCTGCTCTTTTATACCTTCTCTTATATACCT 935
DB 730 CATACTCGTGATCATCGGGCGGTGCTGTTGTTCTACACCATCATCTCATCCCT 789
QY 936 GTATGCGGCTCTCATTTTTTAACGTACTGTCTTCTTATCTTCTTCAAAATGAAGTGA 995
DB 790 GGCTGATCATCTCCTTCATCACTGTGTGCTCTTCTTACCTGCGCTCCGACTGGGTGGA 849
QY 996 AGATTGCTCTGACACTTGTGCTGCTTGTGCTGCTCTTCTGCTCTCTGTTTGAAG 1055
DB 850 AGGTGACCTGTGCAATTTCTGCTCCTCTCTGCTGAGGCTGTTTCTCTGCTGATCACTG 909

1056 AGATCATACCATCATCTTCAAAAGTCATACCTCTAATTCGAGAGATATCTGGTATTTACCA 1115
DB 910 AGACCATCCTTCCACCTCGTGTTCATCCCTGATTGGAGAGTACCTCTCTGTTACCA 969
QY 1116 TGAATTTTGTGACACTGTCAATTATGTTAAACGCTCTTCGCTATCAACATTCATCATGTT 1175
DB 970 TGAATTTTGTAACTTGTCCATCGCCATCACCGTCTTCGTGCTCAACGTCGACTACAGAA 1029
QY 1176 CTTCTCTCAACACATATGCGCGCCCTTTGGTCGCAAGATATTTCTTTCACACGCTTC 1235
DB 1030 CCCCAGGACACACA---CAATGCCCTCATGGTGAAGACTGTATTTCTTGAACCTGCTCC 1086
QY 1236 CCAAACTGCTTTGTCATGAGAATC 1259
DB 1087 CCAGGTCATGTTTCATGACCAGGC 1110

RESULT 11
US-10-349-836-5
; Sequence 5, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; HARPOLD, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 232...2115
; OTHER INFORMATION: alpha4 subunit human neuronal
; nicotinic acetylcholine receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-349-836-5

Query Match	16.6%	Score 303.2	DB 13	Length 3496
Best Local Similarity	59.3%	Prod. No. 7.5e-71		
Matches	575	Conservative	0	Mismatches 383; Indels 12; Gaps 3;
Qy	293	GAAGATAGTTTGGCTTTAAGGATTTTATTTTCAAGACTACGAAGATCGGTTTCGTCTGTGAA	352	
Db	340	GAGGAGCGGCTCTTGAGAAACTCTTTCTCCGGTTACAAACAAGTGTCTCCGACCGGTGCC	399	
Qy	353	CACCTGAATGACAAAATAAAAAATTTTGGACTTGCAATATCTCAATTTGGTGGATGTG	412	
Db	400	AACATCTCGGAGCTGGTCTCGTCCGCTTCGGCTGTCCATCGCTCAGCTCATTTGACGTG	459	
Qy	413	GATGAGAAAATCAGTTTAATGACAAACAACCTCTGTGGTTGAAACAGGAATGATAGATGA	472	
Db	460	GATGAGAAGAACCAAGATGATGACCACGAACGCTATGGGTGAAGCAGGAGTGGCAGACTAC	519	
Qy	473	AAATTAAGATGGAAACCTTGATGACTATGGTGGATAAAGATTATACGTGTTTCCTTCAGAC	532	
Db	520	AAGCTGGCTGGGACCCAGCTGACTATGAGAATGTCACTCCATCGCATCCCTCCGAG	579	
Qy	533	TCTGCTCGGACACGAGCATCGTTTGTTCATAATGCAGATGAGCGTTTGTGAAGGGAC	592	
Db	580	CTCATCTGGCGCCGGACATCGTCTCTAACAATGCTGACGGGACTTCGCGGTCAAC	639	
Qy	593	AGTACGAAAACAGTCATCAGTAGCAAT---GGCACTGTGCACCTGGACTCCACCGGCAAC	649	
Db	640	CACCTGACCAAGGCCACCTGTTCCATGACGGCGGGTGCAGTGGACTCCCGGCCATT	699	
Qy	650	TACAAAAGTTCTGTACCATAGATGTACGTTTTTCCCATTTGACCTTCAGAACTGTGTC	709	
Db	700	TACAAGAGCTCCTGCAGCATCGATGTCACCTTCTTCCCTTCGACCAAGCAACTGCAAC	759	
Qy	710	ATGAAATTTGGTCTCTGACCTTATGATGATCACAGGTTGATATAATCTTAGAGACCA	769	
Db	760	ATGAAATTCGGCTCTCGGACCTACGACGAAGGCAAGATCGACCTGGTGAACATGCACAGC	819	
Qy	770	GATGTAGACAGAGAGATTTTTTTTGCATAATGGGAATGGGAGATTGTGAGTGCAACAGG	829	
Db	820	CGCGTGGACAGCTGGACTTCTGGGAGAGTGGCGAGTGGGTATCTGTGGACCGCTGGC	879	
Qy	830	AGCAAGGAACAGAACCGACAGCTGTGC-----TGGTATCCGTATGTCACTTACTCA	883	
Db	880	ACCTACAAACACAGGAAGTACGAGTGTGCGCGAGATCTACCCGGACATCACCTATGCC	939	
Qy	884	TTTGTATCAAGCGCTGCCTCTTTTATACCTTGTCTTATAATACCTGTATTGGG	943	
Db	940	TTGTCATCGCGGGCTGCCCTCTTCTACACCATCAACCTCATCTCCCTCGCTGCTC	999	
Qy	944	CTCTCATTTTAACTGTACTTGTCTCTATCTCTTCAAAATGAAGGTGAAGACATTGT	1003	
Db	1000	ATCTCTTGCCTCACCGTGTGGTCTTTTACCTGCGCTCCGAGTGTGGGAGAGATCAG	1059	
Qy	1004	CTCTGCACCTTCAGTACTTGTCTTTTGACTGCTTCTCTCTCTGTATTATGAAGAGATCAT	1063	
Db	1060	CTGTGCATCTCCGTGCTGCTGTCTGCTCACCGTCTTCTCTGCTGCTCATCACCGAGATCAT	1119	
Qy	1064	CCATCATCTTCAAAAGTCATACCTCTTAATTTGGAGAGTATCTGTGATTATTCATGATTTT	1123	
Db	1120	CCGTCCACCTCACTGGTTCATCCCACTCATCGCGGAGTACCTGCTGTTCACCATGATCTTC	1179	
Qy	1124	GTGACATGTCAATTATGGTAAACCGTCTTCGCTATCAACATTCATCATCGTTCCTCTCA	1183	
Db	1180	GTCACCTGTCCATCGTCATCACGGTCTTGTGTCTCAACGTCACCAACCGCTCGCCACGC	1239	
Qy	1184	ACACATAATGCCATGGCGCTTTTGGTCCGCAAGATATTTCTTCACAGCTTCCCAAAC	1243	
Db	1240	ACGCACA---CCATGCCCACTGGTAGCAGGGTCTTCTTGGACATCTGTGCCACGCGCTG	1296	
Qy	1244	CTTTGCAATGA	1253	
Db	1297	CTCTCATGA	1306	

RESULT 12

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US-09-878-178-1659/c
; Sequence 1659, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocke, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(296)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-1659

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Query Match

Query Match	16.1%;	Score 295;	DB 10;	Length 296;
Best Local Similarity	99.7%;	Pred. No. 2e-69;		
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Qy	665	ACCATAGATGTCACGTTTTTTCCCATTTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT	724	
Db	296	ACCATAGATGTCACGTTTTTTCCCATTTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT	237	
Qy	725	TGACATTATGATGGATCACAGGTTGTATATAATCTAGAGGACCAAGATGTAGACAAGAGA	784	
Db	236	TGACATTATGATGGATCACAGGTTGTATATAATCTAGAGGACCAAGATGTAGACAAGAGA	177	
Qy	785	GATTTTTTTTGATAATGGAGAATGGAGATTGTGAGTGCACACAGGGACCAAGGAAACAGA	844	
Db	176	GATTTTTTTTGATAATGGAGAATGGAGATTGTGAGTGCACACAGGGACCAAGGAAACAGA	117	
Qy	845	ACCGACAGCTGTTGCTGGTATCCGTATGTCACATTACTCATTTGTAATCAAGCGCTCGCT	904	
Db	116	ACCGACAGCTGTTGCTGGTATCCGTATGTCACATTACTCATTTGTAATCAAGCGCTCGCT	57	
Qy	905	CTCTTTTATACCTTGTTCCTTATAATACCCCTGATTGGGCTCTCATTTTTAACTGT	960	
Db	56	CTCTTTTATACCTTGTTCCTTATAATACCCCTGATTGGGCTCATTTTTAACTGT	1	

RESULT 13

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RES001 13
US-10-046-935-1659/c
; Sequence 1659, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Xuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF COLON CANCER
; FILE REFERENCE: 21021.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1659

Query Match      16.1%; Score 295; DB 14; Length 296;
Best Local Similarity 99.7%; Pred. No. 2e-69;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACCATAGATGTCAGGTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 724
DB 296 ACCATAGATGTCAGGTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 237
QY 725 TGGACTTATGATGATCAGAGTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 784
DB 236 TGGACTTATGATGATCAGAGTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 177
QY 785 GATTTTTTGAATGAGAAATGGAGATTGTGAGTGCAACAGGGAGCAAAAGGAAACAGA 844
DB 176 GATTTTTTGAATGAGAAATGGAGATTGTGAGTGCAACAGGGAGCAAAAGGAAACAGA 117
QY 845 ACCGACAGCTGTGCTGGTATCGTATGTCACCTTCACTTGTATCAATTTGATCAAGCGCTGCCT 904
DB 116 ACCGACAGCTGTGCTGGTATCGTATGTCACCTTCACTTGTATCAATTTGATCAAGCGCTGCCT 57
QY 905 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 960
DB 56 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 1

RESULT 14
US-10-146-502-1659/c
; Sequence 1659, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secret, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Scolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15
; OTHER INFORMATION: n = A,T,C or G
US-10-146-502-1659

Query Match      16.1%; Score 295; DB 15; Length 296;
Best Local Similarity 99.7%; Pred. No. 2e-69;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACCATAGATGTCAGGTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 724
DB 296 ACCATAGATGTCAGGTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 237
QY 725 TGGACTTATGATGATCAGAGTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 784
DB 236 TGGACTTATGATGATCAGAGTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 177
QY 785 GATTTTTTGAATGAGAAATGGAGATTGTGAGTGCAACAGGGAGCAAAAGGAAACAGA 844
DB 176 GATTTTTTGAATGAGAAATGGAGATTGTGAGTGCAACAGGGAGCAAAAGGAAACAGA 117
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QY 845 ACCGACAGCTGTGCTGGTATCGTATGTCACCTTCACTTGTATCAATTTGATCAAGCGCTGCCT 904
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QY 905 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 960
DB 56 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 1

RESULT 15
US-10-157-031-27
; Sequence 27, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-157-031-27

Query Match      16.1%; Score 294.4; DB 15; Length 1667;
Best Local Similarity 58.9%; Pred. No. 1.1e-68;
Matches 568; Conservative 0; Mismatches 381; Indels 15; Gaps 3;

QY 288 AACATGAAGATAGTTTTGCTTAAGGATTTTATTTCAAGACTACGAAAGATGGGTTGCTGCTG 347
DB 113 AACATGAGACCCGCTCTGGTGGCAAGCTATTTAAAGACTACAGACGCGTGGTGGCGCCAG 172
QY 348 TGAACACCTGAAATGACAAAATAAAATAAATTTGGACTTGCATATCTCAATTTGGTGG 407
DB 173 TGAAGACACCGCCAGGTCGTTGGAGGTCACCGTGGGCGCTGCAGCTGATACAGCTCATCA 232
QY 408 ATGTGGATGAGAAAATCAAGTTAATGACAAACAACTCTGTTTGAACAGGAATGATAG 467
DB 233 ATGTGGATGAAGTAATCAGATCGTGACAACTAATGTGCGTCTGAAACAGCAATGGGTGG 292
QY 468 ATGTAATTAAGATGGAACCCCTGATGACTATGGTGGAAATAAAAGTTATACGTTGTTCTT 527
DB 293 ATTACAACCTAATAATGGATCCAGATGACTATGGCGGTGTGAAAAAATTCACATTCTT 352
QY 528 CAGACTCTCTCTGGACACAGACATCGTTTTGTTTGTATTAATGAGATGACAGCTTTTG --- 584
DB 353 CAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACAATGCAGATGGTGTACTTTGCTA 412
QY 585 AAGGGACAGTACGAAAACAGTCATCAGTCAATGGGCACTGTCACCTGCACTCCACCG 644
DB 413 TTGTCAAGTTCCACAAAGTGTCTCTGCACTACATGGCCACATCAGTGGACACCTCCAG 472
QY 645 CAAACTACAAAAGTTCTCTGATACATAGATGTCACTGTTTTCCTCATTTGACCTTCAGAACT 704
DB 473 CCATCTTTAAAGCTACTGTGAGATCATCGTCAACCCACTTTCCCTTTGATGAACAGACT 532
QY 705 GTTCCATGAAATTTGGTTCTTGGACTTATGATGGATCAAGGTTGATATAATTTCTAGAGG 764
DB 533 GCAGCATGAAGCTGGGCACTGAGACCTAGACGGCTCTGTCTGGGCCATCAACCCGAAA 592
QY 765 ACCAGATGTAGACAAGAGAGATTTTTTTGATAATGAGAAATGGGAGATTTGTGAGTGCA 824
DB 593 GCGACCAAGCACTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGAGTCCC 652
QY 825 CAGGGAGCAAGGAAACAGAACCGACAGCTGTTG-----CTGGTATCCGTATGTCA 875
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Db	653	GGGGCTGGAGCACTCCGTGACCTATTCTGCTGCCCGACACCCCTACCTGGACATCA	712
Qy	876	CTTACTCATTTGTAAATCAAGCGCCTGCTCTCTTTTATACCTTGTTCCTTATAATACCCCT	935
Db	713	CCTACCACCTTGGTATGAGCGCCTGCCCTCTACTTCATCGTCAACGTCACTACCCCT	772
Qy	936	GTAATGGGGCTCTCATTTTAACTGTATCTTGTCTTCTATCTTCTTCAAAATGAAGTGAAA	995
Db	773	GCCTGCTCTTCTCTCTTCTTAACTGGCTGTATTTCTACCTGCCACAGACTCAGGGGAGA	832
Qy	996	AGATTGTCTCTGCACTTCAGTACTTGTCTTTTGAAGTCTTCTGCTCTTCTTGGTTATTGAAG	1055
Db	833	AGATGACTCTGAGCATCTCTGCTTACTGTCTTTGACTGTCTCTTCTGCTCATCGTGG	892
Qy	1056	AGATCATACCATCATCTTCAAAAGTCATACCTCTAATTGGAGAGTATCTGGTATTACCA	1115
Db	893	AGCTGATCCCTCCAGTCCAGTCTGTGCTTCTGCTTGGAAATACATGCTGTTACCA	952
Qy	1116	TGATTTTGTGACACTGTCAATATGGTAAACCGTCTTCGCTATCAACATTCATATCGTT	1175
Db	953	TGGTGTGCTGTCATTTGCTTCCATCATCATCTGTCTATCAACACACACACCCGCT	1012
Qy	1176	CTTCCTCAACATATGCAATGGCGCTTTGGTCCGCAAGATATTTCTTACACGCTTC	1235
Db	1013	CACCCAGCACCC---ATGTCATGCCCAACTGGGTCCGGAAGGTTTTTATCGACACTATCC	1069
Qy	1236	CCAA	1239
Db	1070	CANA	1073

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Job time : 1747 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 15:35:42 ; Search time 121 Seconds
(without alignments)
6668.168 Million cell updates/sec

Title: US-09-703-951A-7
Perfect score: 1828
Sequence: 1 CCCGCGGAGCTGTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	557.6	30.5	1925	4	US-08-660-451A-15
4	554.2	30.3	1927	4	US-08-487-596-15
5	554.2	30.3	1927	4	US-08-484-722-15
6	334.6	18.3	2277	1	US-08-496-855A-1
7	334.6	18.3	2277	4	US-08-487-596-1
8	334.6	18.3	2664	4	US-08-660-451A-1
9	324.8	17.8	2068	2	US-08-466-589-1
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11	324.8	17.8	2068	3	US-08-467-574-1
12	324.8	17.8	2068	4	US-09-217-345-1
13	315.6	17.3	1908	4	US-08-660-451A-3
14	314.8	17.2	1743	4	US-08-487-596-9
15	314.8	17.2	1743	4	US-08-484-722-1
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21	303.6	16.6	1654	4	US-08-487-596-3
22	303.2	16.6	3496	4	US-08-660-451A-5
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27	285.2	15.6	2374	2	US-08-700-636-5

28	285.2	15.6	2374	3	US-08-467-574-5
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32	268	14.7	1356	6	5194425-2
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36	237.4	13.0	2448	4	US-08-487-596-13
37	237.4	13.0	2448	4	US-08-660-451A-13
38	237.4	13.0	2450	2	US-08-466-589-9
39	237.4	13.0	2450	2	US-08-700-636-9
40	237.4	13.0	2450	3	US-08-467-574-9
41	237.2	13.0	1915	4	US-09-217-345-9
42	237.2	13.0	1915	4	US-08-487-596-17
43	237.2	13.0	1915	4	US-08-660-451A-17
44	236.8	13.0	1915	1	US-08-496-855A-5
45	236.8	13.0	1915	2	US-08-466-589-11

ALIGNMENTS

RESULT 1
US-08-487-596-7
; Sequence 7, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062


```

GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & Mcclain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 155...1561
OTHER INFORMATION: alpha5 subunit human neuronal
OTHER INFORMATION: nicotinic acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1...154
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1562...1828
OTHER INFORMATION:
US-08-660-451A-7

Query Match 100.0%; Score 1828; DB 4; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CCGCGCGGAGCTGTGGCGCGAGCGGCCCGCTGCTGCGCTCGCTCTGCTTTTGTCTCA 60
DB 1 CCGCGCGGAGCTGTGGCGCGAGCGGCCCGCTGCTGCGCTCGCTCTGCTTTTGTCTCA 60
QY 61 CGACTCACACTCAGTGTGTCATTCCCAAGAGTTTCGGTTTCCCGCGCGCGGTCGAGAG 120
DB 61 CGACTCACACTCAGTGTGTCATTCCCAAGAGTTTCGGTTTCCCGCGCGCGGTCGAGAG 120
QY 121 GCGGCTGCCCGGCTCCCGCGGCGCGGGCGATGCGCGCGCGGGGGTCAGGGGCCCG 180
DB 121 GCGGCTGCCCGGCTCCCGCGGCGCGGGCGATGCGCGCGCGGGGGTCAGGGGCCCG 180

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Qy	181	CGCGCTCCGCCTGCTGCTCTTGGTCTCAGCTGGTTCGCGGGCGCTGCGGTCTAGCGGGCGC	240
Db	181	CGCGCTCCGCCTGCTGCTCTTGGTCTCAGCTGGTTCGCGGGCGCTGCGGTCTAGCGGGCGC	240
Qy	241	GGCGGGCGGCGCGCAGAGAGATTATCTGAACCTTCTTCTATTGCCAAAACTGAAGATAG	300
Db	241	GGCGGGCGGCGCGCAGAGAGATTATCTGAACCTTCTTCTATTGCCAAAACTGAAGATAG	300
Qy	301	TTTGTCTTAAGGATTATTTCAAGACTACGAAAGATGGTTCGTCTGTGGAAACACCTGAA	360
Db	301	TTTGTCTTAAGGATTATTTCAAGACTACGAAAGATGGTTCGTCTGTGGAAACACCTGAA	360
Qy	361	TGCAAAATAAAAAATAAAATTTGGACTTGCATAATCTCAATTGGTGGATGTGGATGAA	420
Db	361	TGCAAAATAAAAAATAAAATTTGGACTTGCATAATCTCAATTGGTGGATGTGGATGAA	420
Qy	421	AAATCAGTTAATGACACAAACGCTCTGGTTGAAACAGGAATGGATAGATGTAAAAATTAA	480
Db	421	AAATCAGTTAATGACACAAACGCTCTGGTTGAAACAGGAATGGATAGATGTAAAAATTAA	480
Qy	481	ATGGAACCCCTGATGACTATGGTGGAAATAAAGTTATACGTGTTCCCTTCAGACTCTGCTG	540
Db	481	ATGGAACCCCTGATGACTATGGTGGAAATAAAGTTATACGTGTTCCCTTCAGACTCTGCTG	540
Qy	541	GACACCCAGACATCGTTTTGTTGATTAATCAGATGGACGTTTTGAAGGGACCACTACGAA	600
Db	541	GACACCCAGACATCGTTTTGTTGATTAATCAGATGGACGTTTTGAAGGGACCACTACGAA	600
Qy	601	AACAGTCATCAGGTACAAATGGCACTGTCACCTGGACTCCACCGGCAAACTACAAAAGTTC	660
Db	601	AACAGTCATCAGGTACAAATGGCACTGTCACCTGGACTCCACCGGCAAACTACAAAAGTTC	660
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Db	781	GAGAGATTTTTTTGATAATGGAGAAATGGGAGATTGTGAGTGCAACAGGGAGCAAGGAAA	840
Qy	841	CAGAACCGACAGCTGTTGCTGGTATCCGATATGCACCTTACTCATTTGCTAATCAAGCGCCT	900
Db	841	CAGAACCGACAGCTGTTGCTGGTATCCGATATGCACCTTACTCATTTGCTAATCAAGCGCCT	900
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Db	901	GCCTCTCTTTATACCTTGTCTCTTATAATACCCCTGTATTGGGCTCTCATTTTAACTGT	960
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Db	961	ACTGTCTCTATCTCTCTTCAAAATGAAGGTGAAAAGATTGTGCTCTGCACTTCAGTACT	1020
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Db	1021	TGTGTCTTTGACTGCTCTCTCTCTGTTATTGAAGAGATCATACCATCATCTTCAAAGT	1080
Qy	1081	CATACCTCTAAATTTGGAGAGTATCTGCTATTACCATGATTTTGTGACACTGCAATTAT	1140
Db	1081	CATACCTCTAAATTTGGAGAGTATCTGCTATTACCATGATTTTGTGACACTGCAATTAT	1140
Qy	1141	GGTAAACGGCTTGGCTATCAACTCATCATCTGTTCTTCTTCAACACATATGCCATGGC	1200
Db	1141	GGTAAACGGCTTGGCTATCAACTCATCATCTGTTCTTCTTCAACACATATGCCATGGC	1200
Qy	1201	GCCTTTGGTCCGCAAGATATTTCTTCCACAGCTTCCCAAACTGCTTTTGCATGAGAAGTCA	1260
Db	1201	GCCTTTGGTCCGCAAGATATTTCTTCCACAGCTTCCCAAACTGCTTTTGCATGAGAAGTCA	1260
Qy	1261	TGTAGACAGAGTACTTCACTCAGAAAGAGGAAAATGAGAGTGTAGTGGACCAAAATCTTTC	1320

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1261 TGAGACAGGACTTCACTCAGAAAGAGAACTGAGGTGGTGTAGTGGACCAAAATCTTC 1320
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1441 GATGTTCTGTCGACATTCCTTTTCGTTTCAATTTGATTCATCTCTGGGCTTTTGTTC 1500
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1681 GCTAACTCAATTTATGTTAAACAGATGATCCATTTGAAGATTCGATGATGATGATGAT 1740
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1801 AGTGAATAATCTAGTATGTTGATCTCTGG 1828
1801 AGTGAATAATCTAGTATGTTGATCTCTGG 1828

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RESULT 3

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US-08-660-451A-15
; Sequence 15, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 98...1474
; OTHER INFORMATION: beta3 human neuronal nicotinic
; OTHER INFORMATION: acetylcholine receptor
; NAME/KEY: 5'UTR
; LOCATION: 1...97
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: 1475...1927
; OTHER INFORMATION:
; US-08-660-451A-15
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; Query Match 30.5%; Score 557.6; DB 4; Length 1925;
; Best Local Similarity 65.2%; Pred. No. 2.9e-137;
; Matches 880; Conservative 0; Mismatches 419; Indels 51; Gaps 2;
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QY 278 TCTATTGCAAAACATGAGATAGTTTGCCTTAAGGATTTATTTCAAGACTACGAAAGATGG 337
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DB 587 CGACGAACTGCTCCATGAAGTTTGGATCTTGACTTATGATGGACCATGTTGACCTC 646
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RESULT 4

US-08-487-596-15

; Sequence 15, Application US/08487596

; Patent No. 6440681

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1927 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 98..1474
OTHER INFORMATION: /product= "BETA-3 SUBUNIT"

US-08-487-596-15

Query Match 30.3%; Score 554.2; DB 4; Length 1927;

Best Local Similarity 66.2%; Pred. No. 2.3e-136;

Matches 858; Conservative 0; Mismatches 388; Indels 51; Gaps 2;

Qy 278 TCTATTGCAAAACATGAAGATAGTTTGTCTTAAGATTATTTTCAAGACTACGAAGATGG 337

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Db 347 GAATGGACAGACCACAAAGTTACGCTGGAATCCTGATGATTATGTGGGATCCATTCCATT 406

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Db 527 ACCCTCCGCGCAGCTACAAAAGCTCTCTGCACCATGACGTCAGCTTTTCCCTGTCGAC 586

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RESULT 5

US-08-484-722-3

; Sequence 3, Application US/08484722

; Patent No. 6485967

; GENERAL INFORMATION:

; APPLICANT: Eliott, Kathryn J.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

```
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,722
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9952
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1927 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 98..1474
OTHER INFORMATION: /product= "BETA-3 SUBUNIT"
US-08-484-722-3
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Query Match 30.3%; Score 554.2; DB 4; Length 1927;

Best Local Similarity 66.2%; Pred. No. 2.3e-136;

Matches 858; Conservative 0; Mismatches 388; Indels 51; Gaps 2;

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Qy 278 TCTATTGCAAAACATGAGATAGTTGCTTAAGGATTTATTTCAAGACTACGAAGATGG 337
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Db 287 CAGCTTGTAGATGTGGATGAAAAAGAAATCAGCTGATGACAAACCAATGTGTGCTCAAAACAG 346
Qy 458 GAATGATAGATGTAAATTTAAGATGGAACCCCTGATGACTATGTTGGAATAAAAGTTATA 517
Db 347 GAATGACAGACACCAAGTTACGCTGGAATCTCTGATGATTTGTTGGGATCCCATTTCCATT 406
Qy 518 CGTGTCTCTTCAGACTCTGCTGACACCAAGATCGTTTGTGATTAATGATGAGATGGA 577
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Qy 635 ACTCCACCGCAAACTACAAAAGTTCTCTGACCATAGATGTCAGCTTTTCCCATTTGAC 694
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QY 1055 GAGATCATACATCTCTCAAAGTCATACCTCTAAATGGAGAGTATCTGTATTTACC 1114
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QY 1115 ATGATTTTGTGACACTGTCAATTAATGTAACCGTCTTCGCTATCAACATTCATCATGT 1174
Db 1007 ATGATTTTGTGACCTGCTGCTCAATGTAACCGTCTTACCGTGTGCTTAACTTCAACAG 1066
QY 1175 TCTTCTCAACATATGCAATGCGCTTTGTCGCAAGATATTTCTTCAACAGCTT 1234
Db 1067 TCTTCTTCCAGTACCAACCCATGCGCTGCTGCTGCTTAAAGAGCTCTTCTGCAAGAACT 1126
QY 1235 CCAAACTGCTTGTGATGAGAGTCAATGTAGACAGTACT----- 1274
Db 1127 CCAAAATTAATTTGATGAAAGATCATGTGATGCTACTCATCCCGAGAGAGAGGAG 1186
QY 1275 -----TCACTCAGAAAGAGGAACTCAGAGTGTAGT 1306
Db 1187 AGTCAACAGTAGTGAAGGCAAGTCTCGAAAGAAAGAAACAGAAACAGCTTAGTAT 1246
QY 1307 GGACCAAAATCTTCTAGAAACATATGGAAGTGGCTCAATTTCTATTCGCTACATTA 1366
Db 1247 GGAGAAAGATTTAGTGTCTTTTGGAAAGCTGCTGATTCATTTAGATACATTTCC 1306
QY 1367 AGACATCATGAAGGAAATGATGCTGCTGAGGTTTGAAGATGGAATTCATAGCC 1426
Db 1307 AGACATGTGAGAAAGAAACATTTTATCAGCCAGGTAGTACAGACTGGAAATTTTGTAGCT 1366
QY 1427 CAGGTTCTGTGCGATGTTCTGTGGACTTTTCTTCTGTTTCAATTTGTTGATCTTT 1486
Db 1367 CAAGTTCTGTGACGAATCTTCTGTGGCTTTTCTGATGCTGCTGCTGCTGCTGCTGCT 1426
QY 1487 GGGCTTTTGTCTGTTTATTTATATAATGGGCAATA 1523
Db 1427 CTGATTTTACCCTGCTTTGAGATGCTGCTACATA 1463

RESULT 6

US-08-496-855A-1

Sequence 1, Application US/08496855A

Patent No. 5801232

GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,855A
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,503
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9369B
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1755
US-08-496-855A-1

Query Match 18.3%; Score 334.6; DB 1; Length 2277;
Best Local Similarity 61.3%; Pred. No. 2.2e-78;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATAGTTTGTCTAAGGATTTATTTCAAGACTACGAAAGATGGGTTCGTCTGTGGA 351
Db 339 TGAGACCGGCTCTTCAACACCTCTTCGCGGGCTACAAACCGCTGGCGCGCGGTGCC 398
QY 352 ACACCTGATGACAAAATAAAATAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db 399 CAACACTTCAGACGCTGGTGTATTGTGCGCTTTGGACTGTCCATCGCTCAGCTCATCATGT 458
QY 412 GGATGAGAAAATCAGTTTAATGACAAACAAAGCTCTGGTTGAAACAGGAATGATAGATGT 471
Db 459 GGATGAGAAACCAATGATGACCAACCAAGCTCTGGCTAAACAGGAGTGGAGGACTA 518
QY 472 AAAATTAAAGATGGAACCTCGATGACTATGTGGGAATAAAAGTTATACGTGTTCTTCTAGA 531
Db 519 CAACCTGCGCTGGAACCCCGCTGATTTGGCAACATCATCATCTCTCAGGGTCCCTTCTGA 578
QY 532 CTCTGTCTGGACACAGACATCGTTTGTGTAATGACAGATGACGTTTGAAGGAC 591
Db 579 GATGATCTGGATCCCGACATTTCTCTACAAACAATGACAGATGGGAGTTTGCAGTGAC 638
QY 592 ---CAGTACGAAACAGTTCATCAGGTACATGGCACTGTCACTGGACTCCACCGGCAAA 648
Db 639 CCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCGCTGGGTCGCGCGGCCAT 698
QY 649 CTACAAAAGTTCTGTACCATAGATGTACACGTTTTCCTTTCACCTTTCAGAACTGTTC 708
Db 699 CTACAGAGCTCTCGAGCATCGACGTCACCTCTTCTCCCTTCGACAGAGACTGCA 758
QY 709 CATGAAATTTGGTCTTGGACTTATGATGAGATCAGGTTGATATAATTTAGAGGACA 768
Db 759 GATGAAATTTGGCTCTCTGGAATTATGACAAAGGCCAAGATCGACCTGGAGCAGATGGAGCA 818
QY 769 AGATGTAGACAGAGATTTTGTGATGAGAGATGGGAGATTTGTGAGTGCACAGG 828
Db 819 GACTGTGGACCTGAAGGACTACTGGGAGAGCGGAGTGGGCCATCGTCAATGCCACGG 878

QY 829 GAGCAAGGAAACAGAACCCAGAGCTGTTGC-----TGGTATCCGTATGTCTACTTACTC 882
Db 879 CACCTACACAGCAAGAGTACGACTCTGCGCGAGATCTACCCCGAGCTCACCTACGC 938
QY 883 ATTGTGAATCAAGCGCTGCTCTTTTATACCTGTTCTCTTATATACCTGATTTGG 942
Db 939 CTTGCTCATCGCGGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCT 998
QY 943 GCTCTCATTTTAACTGACTGTTCTTCTATCTTCTTCTTCAATGAAGGTGAAAGATTG 1002
Db 999 CATCTCTGCTCACTGTGCTGTTCTTCTACCTGCTCCGAGTGGCGGAGAGATCAC 1058
QY 1003 TCTGTGCACTTCAAGTCTGCTGTTGAGTCTTCTTCTGTTATGAGAGATCAT 1062
Db 1059 GCTGTGATTCGCTGCTGCTGCTCACTCACCGTCTTCTGCTGCTCATCATGAGATCAT 1118
QY 1063 ACCATCATCTTCAAAAGTCTATCTTAAATGAGAGATCTGTTATTTACCATGTTT 1122
Db 1119 CCGGTCCACCTGCTGCTGCTATCCGCTCATCGGAGTACCTGTTTACCATGATCTT 1178
QY 1123 TGTGACATCTCAATATGATGTAACCGTCTTTCGCTATCAACATTCATCATGTTCTTCTC 1182
Db 1179 CGTCACCTGCTCATCTGCTATCACCGTCTTCTGCTCAATGTGCACACCGCTCCCCAG 1238
QY 1183 AACACATAATGCCATGCGGCTTGTGTCGCAAGATATTTCTTACACGCTTCCCAAAT 1242
Db 1239 CACCCACA---CCATGCCCACTGGGTGCGGGGGGCGCTTCTGGGCTGTGTGCGCGGTG 1295
QY 1243 GCTTTGCATGA 1253
Db 1296 GCTTCTGATGA 1306

RESULT 7

US-08-487-596-1
; Sequence 1, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1755
OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"
US-08-487-596-1
Query Match 18.3%; Score 334.6; DB 4; Length 2277;
Best Local Similarity 61.3%; Pred. No. 2.2e-78;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATAGTTTGGCTTAAGGATTATTTCAAGACTACGAAAGATGGTTCCTCTGTGGA 351
Db 339 TGAAGACCGGCTCTTCAAAACACCTTTCGGGGTACAAACCGTGGCGGCGCGGTGCC 398
QY 352 ACACCTGAATGACAAAATAAAATTTTGGACTTGGCAATATCTCAATTTGGTGGATGT 411
Db 399 CAACTTCCAGACGCTGCTGATTTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 458
QY 412 GGATGAGAAAATCAGTTAATGACAAACACGCTGCTGTTGAAACAGAAATGGATAGTGT 471
Db 459 GGATGAGAAAGAACAAATGATGACCAACCGCTGCTGGCTTAAACAGAGAGTGGAGCGCTA 518
QY 472 AAAAAATTAAGATGGAACCCCTGATGACTATGTTGGAATAAAAGTTATACGTGTTCTCTCAGA 531
Db 519 CAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA 578
QY 532 CTCTGCTGGACACCAAGACATCGTTTGTGTAATGAGATGGAGCTGTTTGAAGGGAC 591
Db 579 GATGATCTGGATCCCGACATTTGTTCTTCTACAAATGACAGATGGGAGTTTTCAGTGAC 638
QY 592 ---CAGTACGAAAAAGTCAATGAGTACAAATGAGCACTGTCACTGACCTCCACGGGAAA 648
Db 639 CCACATGACCAAGGCCCACTCTTCTCCAGGGCACTGTGCACTGGGTGCCCCGGCCAT 698
QY 649 CTACAAAAGTTCCTGTACCATAGTACGTTTTCCTTCCATTTGACCTTCAGAACTGTTTC 708
Db 699 CTACAAAGAGCTCTCGCAGCATGACGCTCACCTTCTTCCCTTCGACAGCAAGAACTGCAA 758
QY 709 CATGAAATTTGGTCTTCTGGACTTATGATGGATCAGAGTTGATATATTTCTAGAGGACCA 768
Db 759 GATGAAGTTTGGCTCTCGACTTATGCAAGGCCAAGATCGACCTGGAGCAGATGGAGCA 818
QY 769 AGATGTAGACAAGAGATTTTGTGTAATGAGAAATGGAGATTTGTGAGTCAACAGG 828
Db 819 GACTGTGGACCTGAAGGACTTCTGGGAGAGCGCGGAGTGGGCGCATGCTCAATCCACGGG 878
QY 829 GAGCAAGGAAACAGAACCCAGAGCTGTTGC-----TGGTATCCGTATGTCTACTTACTC 882
Db 879 CACCTACACAGCAAGAGTACGACTGCTGCGCGAGATCTACCCCGAGCTCACCTACGC 938
QY 883 ATTGTGAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATATACCTGATTTGG 942
Db 939 CTTGCTCATCGCGGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCT 998
QY 943 GCTCTCATTTTAACTGATCTGTTCTTCTATCTTCTTCTTCAATGAAGGTGAAAGATTG 1002

Db 1568 CGTCACCTGTCCATCGTCATCACCGCTCTTCGTGCTCAATGTGCACCAACCGCTCCCCCAG 1627
Qy 1183 AACACATAATGCCATGGCGCTTGGTCCGCAAGATATTTCTTACACCGCTTCCCAAAT 1242
Db 1628 CACCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG 1684
Qy 1243 GCTTTGCATGA 1253
Db 1685 GCTTCTGATGA 1695

RESULT 9

US-08-466-589-1
; Sequence 1, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 166..1752
; US-08-466-589-1

Query Match 17.8%; Score 324.8; DB 2; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;
Qy 292 TGAAGATAGTTGCTTAAAGATTTATTCAAGACTACGAAGATGGGTTCGTCTGTGGA 351
Db 339 TGAGGACCGGCTCTTCAACACCTCTTCCGGGGCTACAAACCGCTGGCGCGCGCGTGC 398
Qy 352 ACACCTGAATACAAAATAAAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db 399 CAACACTTCAGACGTGGTGAATTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATG 458

Qy 412 GGATGAGAAAAATCAGTTAATGACAAACAAACGTCTGGTTGAAACAGGAATGGATAGATGT 471
Db 459 GGATGAGAAAGAACAAATGATGACCAACCAACGTCTGGCTTAAACAGGAGTGGAGCGCA 518
Qy 472 AAAATTAGATGGAAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
Db 519 CAAACTGCGCTGGAAACCGCGCTGATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578
Qy 532 CTCTGTCTGGACACCAAGACATCGTTTGTGATGATGATGATGATGATGATGATGATGATG 591
Db 579 GATGATCTGGATCCCGACATTTGTTCTTACAAANNTGGGAGTTGTCAGTGACCCA 638
Qy 592 CAGTACGAAAAAGTCAATCAGGTACAAATGGCACTGTCACTGGACTCCACCGGCAAACTA 651
Db 639 CATGACCAAGGCCACCTCTTCCACGGGCACTGTGCATCGGTGCGCGCCCATCTA 698
Qy 652 CAAAAGTTCTGTACCATAGATGTACAGTTTTCCTTCCATTTGACCTTCACAACTGTTCCAT 711
Db 699 CAAGAGCTCTCGACATCGACGTCACTTCTTCCCTTCGACCAAGCACTGCAAGAT 758
Qy 712 GAAATTTGGTCTTGGACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db 759 GAAGTTTGGCTCTGGACTTATGACAAAGCCAAAGATCGACCTGGAGCAGATGGAGCAG 818
Qy 772 TGTAGACAAAGAGAGATTTTTTTGATTAATGGAGATGGAGATGTGAGTGCACAGGGAG 831
Db 819 TGTGGACCTGAAGGACTACTGGGAGAGCGCGGAGTGGGCGCATCGTCAATGCGACGGGC 878
Qy 832 CAAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTCAT 885
Db 879 CTACAAACAGCAAGAGTACGACTGTCTGCGCCGAGATCTTACCCCGACGTCACTTACGCT 938
Qy 886 TGTAAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATATAATACCTGTATTTGGGCT 945
Db 939 CGTATCCCGGGCTGCGCTCTTCTACACATCAACCTCATCATCTCTCTGCTGCTCAT 998
Qy 946 CTCATTTTAACTGTACTTGTCTTCTATCTTCTTCAATGAAGGTGAAAAGATTTGTCT 1005
Db 999 CTCCTGCCCTCACTGTGTGTCTTCTTACCTGCGCTCGGAGTGGGAGAGATCACGCT 1058
Qy 1006 CTGCACTTCACTGTGTGTCTTGTGACTGTCTCTCTCTCTCTGTTTATTGAAGAGATCAT 1065
Db 1059 GTGCATTTCTGCTGTCTGTCTCACTACCGCTTCTCTGCTGCTCATCACTGAGATCATCC 1118
Qy 1066 ATCATCTTCAAAAGTCACTACCTCTAATTTGAGAGATATCTGGTATTACCATGATTTTGT 1125
Db 1119 GTCCACTCGTGTGTATCCCGCTCATCGGCGAGTACCTGTCTTCCATCATGATCTTGT 1178
Qy 1126 GACACTGTCAATATATGTAACCGCTTTCGCTATCAACATTCATCATCTTCTTCTCAAC 1185
Db 1179 CACCTGTCCATGCTCATCACCGCTTTCGTGCTCAATGTGGACCAACCGCTCCCCCAGC 1238
Qy 1186 ACATAATGCCATGGCGCTTGTGTCGCGAAGATATTTCTTCAACGCTTCCCAAACTGCT 1245
Db 1239 CCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTTGGGCTGTGTGCGCGGTG 1295
Qy 1246 TTGCATGA 1253
Db 1296 TGTGATGA 1303

RESULT 10

US-08-700-636-1
; Sequence 1, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 166...1752
US-08-700-636-1

Query Match 17.8%; Score 324.8; DB 2; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;

QY 292 TGAAGATAGTTGCTTAAGATTATTTCAAGACTACGAAAGATGGTTCCTGTGGA 351
DB 339 TGAGGACCGGCTCTTCAACACCTCTTCGGGGCTACAAACCGCTGGGGCGCCGCGCC 398
QY 352 ACACCTGAATGACAAATAAATAATTTGGACTTGCATATCTCAATTGGTGGATGT 411
DB 399 CAACACTTCAGACGTGGTGAATTTGGCTTTGGACTGTCCTCAGCTCAGCTCATCGATGT 458
QY 412 GGATGAGAAATATCAGTTAATGACAAACAAACCTCTGGTTGAAACAGGAATGGATAGATGT 471
DB 459 GGATGAGAAACCAAAATGATGACCAACCAACCTCTGGCTTAAACAGGAGTGGAGGACTA 518
QY 472 AAAATTAAGATGGAACCTGATGACTATGTTGGAAATAAAGTTATACGTTCCTTCAGA 531
DB 519 CAAACTGGCTGGAACCCCGCTGATTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578
QY 532 CTCTCTGGACACGACATCGTTTGTGTTGATATGACATGACATGTTTGAAGGAC 591
DB 579 GATGATCTGGATCCCGCAATGTTCTCTACAAACAAANNWGGGAGTTTGCAGTGACCCA 638
QY 592 CAGTACGAAAAACAGTCATCAGGTACAAATGGCACTGTCCACTGGACTCCACCGGCAAACTA 651
DB 639 CATGACCAAGGCCACCTCTTCTCACGGGCACTGTGCACTGGGTGCCCCCGGCATCTA 698
QY 652 CAAAAGTTCCTGATACATAGATGTCAGTTTTCCTCCATTTGACCTTCAGAACTGTTCAT 711
DB 699 CAAAGAGCTCTCAGCATCGACGTCACTCTTCTCCCTTCGACCAAGCAAGTCAAGAT 758
QY 712 GAAATTTGGTCTTGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 771
DB 759 GAAATTTGGCTCTGAGCTTATGACAAAGGCCAAGATCGACCTGGGAGCAGATGGAGCAGAC 818

QY 772 TGTAGACAAGAGAGATTTTTTTTGATAATGGAGAAATGGAGAGATTGTGAGTCAACAGGGAG 831
DB 819 TGTGACCTGAAGGACTACTGGGAGAGCGGAGTGGGCCATCGTCAATGCCACGGGCAC 878
QY 832 CAAAGGAAACAGAACCGACAGCTGTGC-----TGGTATCCGTATGTCACTTACTTCAAT 885
DB 879 CTACAAACAGCAAGAGTACGACTGTGCGCCGAGATCTACCCCGACGTCACCTAGCCTT 938
QY 886 TGTAAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATAATACCTCTGTATTGGGCT 945
DB 939 CGTCATCCGGCGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCTCAT 998
QY 946 CTCAATTTTAACTGTACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005
DB 999 CTCTGCTCTCACTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1058
QY 1006 CTGCACTTCACTACTGTGTCT 1065
DB 1059 GTGCATTTCCGT 1118
QY 1066 ATCATCTTTCAAAAGTCATACCTCTAAATTTGAGAGATATCTGGTATTTTACCATGATTTTGT 1125
DB 1119 GTCCACCTGCTGT 1178
QY 1126 GACACTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
DB 1179 CACCTGTGCTCATCGTCATCACCGCTCTTCTGTCTCAATGTGACCAACCGCTCCCCAGC 1238
QY 1186 ACATAATGCCATGGCGCTTTGGTCCGCAAGATATTTCTTCAACAGCTTCCCAACTGCT 1245
DB 1239 CCACA---CCATGCCCACTGGGTGCGGGGGGGCCCTTCTGGGCTGTGTGCCCCCGTGGCT 1295
QY 1246 TTGCATGA 1253
DB 1296 TCTGATGA 1303

RESULT 11

US-08-467-574-1
Sequence 1, Application US/08467574
Patent No. 6022704
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1752
US-08-467-574-1

Query Match 17.8%; Score 324.8; DB 3; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;
QY 292 TGAAGATAGTTGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCTGCTCTGGGA 351
Db |||||
QY 339 TGAGGACCGGCTCTTCAACACCTCTTCGGGGCTACACCGCTGGCGCGCGGTGCC 398
Db |||||
QY 352 ACACCTGAATGACAAATAAAATTTGGACTTGCATATCTCAATGGTGGATGT 411
Db |||||
QY 399 CAACACTTCAGCGTGGTGTGTTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 458
QY 412 GGATGAGAAAATCAGTTAATGACAAACAAACGCTGCTGTTGAAACAGGAATGGATAGATGT 471
Db |||||
QY 459 GGATGAGAGAACCAATGATGACCAACAGCTGCTGCTTAACAGAGATGGAGCGACTA 518
QY 472 AAAATTGAATGGAACCTGATGACTATGTTGGAATAAAAGTTATACGTTCTCTTCAGA 531
Db |||||
QY 519 CAAACTCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGCTCCCTCTGA 578
QY 532 CTCTGCTGGACACCAACATCGTTTGTGTTGTAATGACAGATGGAGCTTTTGAAGGAC 591
Db |||||
QY 579 GATGATCTGATCCCGACATGTTCTCTACAAANNTGGGAGTTTCAGTGAACCA 638
QY 592 CAGTACGAAACAGTCAATCAGGTACATGACCTGACCTGACCTGACCTCCACCGGCAACTA 651
Db |||||
QY 639 CATGACCAAGGCCACCTCTCTCCAGGGGACATGTCATGTTGGTGGCCCGGCGCATCTA 698
QY 652 CAAAGTTCTCTGATACCATAGATGTCAGCTTTTCCCAATTTGACCTTCAGAACTGTTCCAT 711
Db |||||
QY 699 CAAGAGCTCTGACGATCAGCTGCTCTCTTCCCTTCGACCAAGCAACTGCAAGAT 758
QY 712 GAAATTTGGTCTTGGACTATGATGATCAGAGTTGATATAATTTAGAGGACCAAGA 771
Db |||||
QY 759 GAATTTGGTCTCTGAGCTTATGACAGGCGCAAGATCGACCTGGAGCAGATGGAGCAGAC 818
QY 772 TGATGACAGAGAGATTTTGTGATAATGGAGATGGAGATGTTGAGTGCACAGGGAG 831
Db |||||
QY 819 TGTGGACTGAGGACTACTGGGAGCGGGAGTGGGCCATCTCAATGCCAGGGCAC 878
QY 832 CAAAGGAAACAGAACCGACAGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
Db |||||
QY 879 CTACACAGCAAGAGTACGACTGCTGCGCGAGATCTACCCGACGCTACCTAGGCTT 938
QY 886 TGTAAATCAAGCGCTGCTCTCTTTTATACCTGTTCTTTATATACCTGATTTGGGCT 945
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QY 939 CGTCACTCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATCTCCCTGCTGCTCAT 998
QY 946 CTCAATTTTAACTGCTACTGCTCTCTATCTCTCTTCAATGAAAGTCAAAAGATTTTCT 1005
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QY 999 CTCCTGCTCACTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1058
QY 1006 CTGCACTTCAGTACTTGTGCTTTGACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1065
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QY 1059 GTGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
QY 1066 ATCATCTTCAAAAGTCACTACTCTAAATTTGGAGAGTATCTGTTATTTACCATGATTTTGT 1125
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QY 1126 GACACTGTCAATATAGTAAACCGTCTTCGCTATCAACATTCATCATCGTTTCTCTCAAC 1185
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QY 1179 CACCTGTCCATCGTTCATCAGCGTCTTCGTGCTCAATGTGGACCAACCGCTCCCCCAGCAC 1238
Db |||||
QY 1186 ACATAATGCCATGGCGCTTTGGTCCGCAAGATATTTCTTCACACGCTTCCCAACTGCT 1245
Db |||||
QY 1239 CCACA---CCATGCCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCGGTGGCT 1295
Db |||||
QY 1246 TTGCATGA 1253
Db |||||
QY 1296 TCTGATGA 1303

RESULT 12
US-09-217-345-1
Sequence 1, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA: US 08/467,574
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA: US 08/466,589,
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA: US 08/028,031
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1752
US-09-217-345-1

Query Match 17.8%; Score 324.8; DB 4; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;

QY 292 TGAAGATAGTTTGGCTTAAGGATTATTTCAAGACTACGAAGATGGGTTCTGCTGTGGA 351
Db |||||
QY 339 TGAGGACGGCTCTTCAAAACACCTCTTCGGGGCTTACAAACCGCTGGCGCGCGGTCGCC 398
Db |||||
QY 352 ACACCTGAATGACAAAATAAAATTTGGACTTGGCAATATCTCAATGCTGGATGT 411
Db |||||
QY 399 CAACACTTCAGAGGTGGTGAATTTGGGCTTTGGACTGTCCATCGCTCAGCTCATGTG 458
Db |||||
QY 412 GGATGAGAAAATCAGTTAATGACAAACAAACCTCTGTTGTAAGAGGAATGGATGATGT 471
Db |||||
QY 459 GGATGAGAAACCAAAATGATGACCAACCAACCTCTGGCTTAAACAGGAGTGGAGGACTA 518
Db |||||
QY 472 ARAATTAAGATGGAACCTGTGACTATGTTGGAATAAAGTTATACGTTCTCTCAGA 531
Db |||||
QY 519 CAACCTGGCTGGAACCGCGCTGATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578
Db |||||
QY 532 CTCTGCTGACACGACGACATCGTTTGTGTAATGAGATGACAGCTGTTTGAAGGAC 591
Db |||||
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Db |||||
QY 639 CATGACCAAGGCCACCTCTTCTCACGGGCACTGTGCACTGGGTGCCCCGGCCATCTA 698
Db |||||
QY 652 CAAAAGTTCCTGTACATAGATGTCACTTTTCCATTTGACCTTCAGAACTGTTCAT 711
Db |||||
QY 699 CAAGAGCTCTGACGATGAGCTGACCTTCTTCCCTTCGACGACGAGAACTGAAGT 758
Db |||||
QY 712 GAAATTTGGTCTCTGACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db |||||
QY 759 GAAGTTGGCTCTGACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 818
Db |||||
QY 772 TGTAGACAGAGAGATTTTGTGTAATGAGAGATGGGAGATTTGAGTGCAACAGGAG 831
Db |||||
QY 819 TGTGACCTGAAGGACTCTGGGAGAGCGGAGTGGCCATCGTCAATGCCACGGGAC 878
Db |||||
QY 832 CAAAGGAAACAGAACCGACAGCTGTGTC-----TGGTATCGGTATGCTACTTACT 885
Db |||||
QY 879 CTACACAGCAGAAAGTACGACTGTGCGCGGAGATCTACCCGACGTCACCTAGCGCT 938
Db |||||
QY 886 TGAATATCAAGCGCTGCTCTCTTTTATACCTGTTCTTATATACCTGTATGGCT 945
Db |||||
QY 939 CGTCATCGCGCGCTGCGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCTCAT 998
Db |||||
QY 946 CTCAATTTTAACTGTAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005
Db |||||
QY 999 CTCTGCTCTACTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1058
Db |||||
QY 1006 CTGCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065
Db |||||
QY 1059 GTGCAATTTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
Db |||||
QY 1066 ATCATCTTCAAAAGTCATACCTCTAAATTTGGAGAGTATCTGTTATTTAGCATGTTTGT 1125
Db |||||
QY 1119 GTCCACCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
Db |||||
QY 1126 GACACTGTCAATTTATGTAACCGTCTCTGCTATCAACATTCATCTCTCTCTCTCTCTCT 1185
Db |||||
QY 1179 CACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1238
Db |||||
QY 1186 ACATTAATGCGATGGCGCTTTGGTCCGCAAGATATTTCTTCAACGCTTCCCAACTGCT 1245
Db |||||
QY 1239 CCACA---CCATGCCCACTGGGTGCGGGGGGCGCTTCTGCGCTGTGTGCGCGGTGCT 1295
Db |||||
QY 1246 TTGCATGA 1253
Db |||||
QY 1296 TCTGATGA 1303

RESULT 13
US-08-660-451A-3
; Sequence 3, Application US/08660451A
; Patent No. 6524789

GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 190...1704
OTHER INFORMATION: alpha3 subunit human neuronal
OTHER INFORMATION: nicotinic acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1...189
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1705...1908
OTHER INFORMATION:
US-08-660-451A-3

Query Match 17.38; Score 315.6; DB 4; Length 1908;
Best Local Similarity 59.8; Pred. No. 2e-73;
Matches 588; Conservative 0; Mismatches 384; Indels 12; Gaps 3;
QY 285 CAAACATCAAGATGATGTTTCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCTGTC 344
Db |||||
QY 345 CTGTGGAAACCTGGAATGACAAAATAAAATTTGGACTTTGCAATATCTCAATG 404
Db |||||
QY 341 CTGTAGCCAAACGCTGCTGACCCAGTCATCATCTTCGAGGTGCTCCATGCTCAGCTGG 400
Db |||||
QY 405 TGGATGTGGATGAGAAAATCAGTTAATGACAAACAAACCTCTGGTTGAAAACAGGAATGA 464
Db |||||
QY 401 TGAAGGTGGATGAAGTAACCAACCATGATGAGAGCAACCACTGTGCTCAAGCAATCTGGA 460

Db 541 AGGCAAAACAAAGCTCTTCTTAATACATGCGATGATACCTGGACTCCACAGCTAT 600
Qy 649 CTCACAAAGTTCCTGTACATAGATGTCAAGTTTTTCCCATTTGACCTTCAGAACTGTTC 708
Db 601 TTTTAAAGAGTTCCTGCCCTATGATATCACCTTTTTTCCCTTTGATCATCAAACTGTTC 660
Qy 709 CATGAAATTTGGTTCCTGGACTTATGATGATGATCACAGTTGATATTAATCTAGAGGACA 768
Db 661 CCTAAATTTGGTTCCTGGAGATGACAAAGCTGAAATTTGATCTTCAATCATTTGGATC 720
Qy 769 AGATGTAGACAGAGAGATTTTTTGTATAATGAGAGTGGAGATTTGGAGTGCAACAGG 828
Db 721 AAAAGTGATATGATGATTTTTTGGGAAACAGTGAATGGGAAATCATTTGATGCTCTGG 780
Qy 829 GAGCAAAAGGAAACAGAACCGACGCTGTG-----CTGGTATCGTATGTCATCTACTC 882
Db 781 CTCACAAACATGATACATCAAACTGTTGTGAAGAGATATACAGATATAACCTATTTC 840
Qy 883 ATTTGTAATCAAGCGCTGCTCTCTTTATACCTTTGTTTATTAATACCTGTATTTGG 942
Db 841 TTTCTACATTAAGAGATTTGCCGATGTTTACAGGATTAATCTGATCATCTCTGTCTCT 900
Qy 943 GCTCTCATTTTAACTGTACTGTCTTCTATCTTCTCAATGAAGTGAAGATTTG 1002
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Qy 1003 TCTGTCACTTCAGTACTGTCTTGTGACTGTCTTCTCTCTGTTATTTGAAGAGATCAT 1062
Db 961 GCTTTGATTTCAAGTCTGCTTCTCTGACTGTGTTTTTGTGTTGTCATACAGAAACCAT 1020
Qy 1063 ACCATCATCTTCAAAAGTCATACCTCTTAATTTGGAGAGTATCTGTGTTATTTACATGATTTT 1122
Db 1021 CCCATCCACATCTCTGTGTGGTCCCACTGTGGTGTGAGTACCTGCTGTTTCAACCATGATCTT 1080
Qy 1123 TGTGACACTGCAATTTATGTTAAGCTCTTCTGCTATCAAGTTCATCATCTGTTCTCTC 1182
Db 1081 TGTCACTGTCCATCGTGGTGTGCTGTTGTTGTTGAACATACACTACCGACCCCAAC 1140
Qy 1183 AACCATATGTCATGCGGCTTTTGGTCCGCAAGATATTTCTTCAACGCTTCCCAACT 1242
Db 1141 CAGGCACA--CAATGCCAGGTGGTGAAGACAGTTTTCTGAGCTGTGCCCCAGGT 1197
Qy 1243 GCTTTGATGAGAGTCAATGATAGACAGG 1270
Db 1198 CTTGCTGATGAGTGGCTCTGGACAAG 1225

RESULT 15

US-08-484-722-1
; Sequence 1, Application US/08484722
; Patent No. 6485967
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,722
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9952
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..1627
; OTHER INFORMATION: /product= "ALPHA-6 SUBUNIT"
; US-08-484-722-1

Query Match 17.2%; Score 314.8; DB 4; Length 1743;
Best Local Similarity 59.6%; Pred. No. 3.2e-73;
Matches 589; Conservative 0; Mismatches 387; Indels 12; Gaps 3;
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Db 241 TGAGGAGAGGCTCTTCCCAAACTGTTTTCTCATTAACAACCACTTCATCAGGCCCTGTGGA 300
Qy 352 ACACCTGAATGACAAAATAAAATTTGGACTTTGGACTATCTCAATTTGGTGGATGT 411
Db 301 AAACGTTTCCGACCTGTCCAGGTACACTTTTGAAGTGGCCCATCACCCAGCTGGGCCAACGT 360
Qy 412 GGATGAGAAAATCAGTTAATGACAAACAACTCTGTTGTAACAGGAATGGATAGATGT 471
Db 361 GGATGAGTAAACAGATCATGGAACCAATTTGTGGCTGCGTCACATCTGGAATGATTA 420
Qy 472 AAAATTAAGATGGAACCTGATGACTATGTGGGAAATAAAAGTTATACGTGTCTTCTCAGA 531
Db 421 TAAATTCGCTGGGATCCAATGGAATATGATGGCATTTGAGACTCTTGGCGTTCTCTGAGA 480
Qy 532 CTCTGTCTGGACACCAGACATCGTTTGTGTTGTAATGACAGATGGAGCTTT--TGAAGG 588
Db 481 TAAGATTTGGAAGCCCGACATTTGTTCTTATAAATGCTGTGTTGTTGCTGACTTCCAAGTAGA 540
Qy 589 GACCAGTACGAAACAGTCACTCAGGTACAAATGGGACTGTCACTGGACTCCACCGGCAAA 648
Db 541 AGGCAAAACAAAGCTCTTCTTAATACATGGAATGATACCTGGACTCCACAGCTAT 600
Qy 649 CTACAAAAGTTCTGTACCATAGATGTCAAGTTTTTCCCATTTTGGACCTTCAGAACTGTTC 708
Db 601 TTTTAAAGAGTTCCTGCCCTATGATATCACCTTTTTTCCCTTTTGCATCATCAAAACTGTTC 660
Qy 709 CATGAAATTTGGTTCCTTGGACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 768
Db 661 CCTAAATTTGGTTCCTTGGAGCTGATGACAAAGCTGAAATTTGATCTTCTTAATCATTTGGATC 720
Qy 769 AGATGTAGACAGAGAGATTTTTTGTATAATGAGAGTGGAGATTTGGAGTGCAACAGG 828
Db 721 AAAAGTGATATGATGATTTTTTGGGAAACAGTGAATGGGAAATCATTTGATGCTCTGG 780
Qy 829 GAGCAAAAGGAAACAGAACCGACGCTGTG-----CTGGTATCGTATGTCATCTACTC 882
Db 781 CTCACAAACATGATACATCAAACTGTTGTGAAGAGATATACAGATATAACCTATTTC 840
Qy 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTCTTATTAATACCTGTATTTGG 942
Db 841 TTTCTACATTAAGAGATTTGCCGATGTTTACAGGATTAATCTGATCATCTCTGTCTCTT 900
Qy 943 GCTCTCATTTTAACTGTACTGTCTTCTATCTTCTTCAATGAAGTGAAGATTTG 1002
Db 901 TATTTCAITTTAAACCGTGTGGTCTTTTACCTCTTCGGACTGTGGTGAAGAGTGAC 960
Qy 1003 TCTGTCACTTCAGTACTGTGTTGTTGACTGTCTTCTCTCTGTTATTTGAAGAGATCAT 1062

961	db	GCTTTGTTATTTCTGAGTCTCTGCTTTCTCTGACTGTTTTTCTGGTGCATCAGAGAACCAT	1020
1063	Qy	ACCATCATCTTCAAAGTCATACCTCTAAATTGGAGAGTATCTGGTATTTACCATGATTTT	1122
1021	Db	CCATCCACATCTCTGGTGGTCCCACTGGTGGGTGAGTACCTGCTGTTCCACATGATCTT	1080
1123	Qy	TGTGACACGTGCAATPATGTTAAACCGTCTTCGTATCAACATTCATCATCTGTTCTTCCCTC	1182
1081	Db	TGTCACTGTCCATCGTGGTGACTGTGTTGTGTGAACATACACTACCGCACCCCAAC	1140
1183	Qy	AACACATAATGCCATGGCGCCTTTGGTCGCGAAGATATTTCTTCACACGTTCCCAACT	1242
1141	Db	CACGCACA---CAATGCCAGGTGGGTGAAGACAGTTTTCTTGAAGCTCTGCCCCAGGT	1197
1243	Qy	GCTTTGCATGAGAAGTCATGTAGACAGG	1270
1198	Db	CTGTGCTGATGAGTGGCCTCTGGACAAG	1225

Search completed: December 23, 2003, 15:38:12
Job time : 131 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 15:35:43 ; Search time 523 Seconds
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Perfect score: 1828
Sequence: 1 CCCGCGGAGACTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	1828	18 AAT48238	Neuronal nicotinic
2	1828	100.0	1828	24 ABV73246	Human neuronal NAC
3	1828	100.0	1828	24 ABS54873	Human neuronal nic
4	557.6	30.5	1925	18 AAT48234	Neuronal nicotinic
5	555.8	30.4	1377	22 AAD20828	Human CHRN3 gene
6	554.2	30.3	1927	24 ABV73250	Human neuronal NAC
7	554.2	30.3	1927	24 ABS54877	Human neuronal nic
8	377.6	20.7	1638	22 AAD20826	Human CHRN3 parti

9	377.6	20.7	1638	22	AAD20870	Human CHRN3 parti
10	334.6	18.3	2277	15	AAV12199	Human neuronal nic
11	334.6	18.3	2277	16	AAQ90387	Alpha 2 subunit of
12	334.6	18.3	2277	24	ABV73243	Human neuronal NAC
13	334.6	18.3	2277	24	ABS54870	Human neuronal nic
14	334.6	18.3	2664	18	AAT48235	Neuronal nicotinic
15	334.6	18.3	2664	24	ABK92165	Prostate cancer-as
16	315.6	17.3	1908	18	AAT48236	Neuronal nicotinic
17	314.8	17.2	1743	18	AAT48232	Neuronal nicotinic
18	314.8	17.2	1743	24	ABV73247	Human neuronal NAC
19	314.8	17.2	1743	24	ABS54874	Human neuronal nic
20	304.8	16.7	2082	18	AAT59527	Alpha4 subunit of
21	303.6	16.6	1654	24	ABV73244	Human neuronal NAC
22	303.6	16.6	1654	24	ABS54871	Human neuronal nic
23	303.6	16.6	1757	15	AAV12200	Human neuronal nic
24	303.2	16.6	1809	23	AAS91552	DNA encoding novel
25	303.2	16.6	2082	18	AAT59528	Alpha4 subunit of
26	303.2	16.6	3496	18	AAT48237	Neuronal nicotinic
27	296.2	16.2	299	24	ABL38070	Human colon tumour
28	294.4	16.1	1667	21	AAZ38821	Human acetylcholin
29	293.6	16.1	3649	6	AAN50416	Calf acetyl cholin
30	291.4	15.9	1350	17	AAT06284	Acetylcholine rece
31	290.4	15.9	2363	15	AAV12196	Human neuronal nic
32	290.4	15.9	2363	24	ABV73245	Human neuronal NAC
33	290.4	15.9	2363	24	ABS54872	Human neuronal nic
34	289.8	15.9	1350	14	AAQ35053	Alpha subunit of T
35	289	15.8	1350	14	AAQ39941	Acetylcholine rece
36	280.8	15.4	1869	24	AAI45873	Modified acetylcho
37	280.8	15.4	1869	24	ABL54794	Modified hen ACR s
38	270.6	14.8	1698	18	AAT48233	Nicotinic acetylch
39	269.2	14.7	1350	15	AAQ56918	Acetylcholine rece
40	261.4	14.3	1896	24	AAI45870	Modified acetylcho
41	261.4	14.3	1896	24	ABL54791	Modified hen ACR s
42	260	14.2	1869	24	AAI45864	Modified acetylcho
43	260	14.2	1869	24	ABL54788	Insect nicotinic A
44	244.8	13.4	2460	11	AAQ06086	Plasmid pZPC13 enc
45	239	13.1	1521	12	AAQ14288	Human neuronal nic

ALIGNMENTS

RESULT 1

AAT48238
ID AAT48238 standard; DNA; 1828 BP.

XX AAT48238;

AC AAT48238;

DT 09-APR-1997 (first entry)

DE Neuronal nicotinic acetylcholine receptor alpha-5 subunit DNA.

XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

KW ligand-gated receptor; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 155..1561

FT /*tag= a

PN WO9641876-A1.

XX 27-DEC-1996.

XX 07-JUN-1996; 96WO-US09775.

XX 07-JUN-1995; 95US-0484722.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Harpold WM;

Query Match	100.0%;	Score 1828;	DB 24;	Length 1828;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1828;	Conservative	0;	Mismatches	0;	Gaps
Qy	1	CCCGCGGAGCTGTGGCGCGAGCGGCCCGCTGCTGCGTCTGCCCTCGTTTGTCTCA	60		
Db	1	CCCGCGGAGCTGTGGCGCGAGCGGCCCGCTGCTGCGTCTGCCCTCGTTTGTCTCA	60		
Qy	61	CGACTCACACTCAGTGTGCAATCCCAAGAGTTTCGGCTTCCCGCGCGCGGTGAGAG	120		
Db	61	CGACTCACACTCAGTGTGCAATCCCAAGAGTTTCGGCTTCCCGCGCGCGGTGAGAG	120		
Qy	121	GGCGTGTCCCGTCCCGCGCGCGCGGGGCGATGCGGGCGGGGGTCAAGGGCCCCG	180		

CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3
CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is coding region
CC of human CHRN3 gene. Human CHRN3 gene includes 8 polymorphic sites.
CC PS1-PS8.
XX
SQ Sequence 1377 BP; 370 A; 323 C; 283 G; 401 T; 0 other;

Query Match 30.4%; Score 555.8; DB 22; Length 1377;
Best Local Similarity 66.2%; Pred. No. 6.2e-125;
Matches 859; Conservative 0; Mismatches 387; Indels 51; Gaps 2;

QY 278 TCTATTGCAAAACATGAAGATAGTTTGTCTTAAGGATTTATTCAAGACTACGAAAGATGG 337
DB 70 TCAATCGCGAANAATGAAGATGCCCTCTCAGACATTTGTTCGAAGTTATCAGAAATGG 129
QY 338 GTTCGTCCTGTGGAAACACCTGAATGACAAAATAAATAAATTTGGACTTTGCAATATCT 397
DB 130 GTCCGCCCTGTATTACATTTCTAATGACACCAATAAAGTATATTTGGATTGAATATCC 189
QY 338 CAATTGGTGGATGTCGATGAGAAAATCAGTTAATGACAAACAACTGTGGTTGAAACAG 457
DB 130 CAGCTTGTAGATGTCGATGAAAGAAATCAGCTGATGACAAACAAATGTGTGGCTCAAACAG 249
QY 458 GAATGGATAGATGTAATAATTAGATGGAACCTGATGACTGATGGTGAATAAAGTTATA 517
DB 250 GAATGGACAGACCACAAGTTACGCTGGAAATCTCTGATGATTAATGGTGGGATCCATTC 309
QY 518 CGTGTCTCTCAGACTCTGTCTGGACACAGACATCGTTTGTGTTGTAATGACAGATGGA 577
DB 310 AAGATTCCATCAGATCTCTGTGGCTCTCTGACATAGTTCTTTTGAATAAGTCTGACGCG 369
QY 578 GCTTTTGAAGGACACGATGACGAAACAGTCATC---AGGTACAATGGCACTGTCACTGG 634
DB 370 CGCTTCGAAGGCTCCCTGATGACCAAGGTCATCGTGAATCAACGGAACGTGTCTCTGG 429
QY 635 ACTCCACGGCAAACTACAAAGTTCCGTACCATAGATGTCACGTTTTCCTCATTTGAC 694
DB 430 ACCCTCCCGCAGCTACAAAGCTCCCTGCACCATGGACGTACACGTTTTCCTCGTTCAC 489
QY 695 CTTGAGAACTGTTCATCAAAATTTGGTCTTGGACTTATGATGATGATCAGAGTTTCAATA 754
DB 490 CGACAGAACTGCTCATGAGTTTGGATCTCTGACTTATGATGACCATGTTGACCTC 549
QY 755 ATTCTAGAGGACCAAGATGTAGACAAAGAGATTTTGTGATAATGGAGATGGAGATT 814
DB 550 ATTTTGTATCAATGAAATGTGACAGAAAAGACTTCTTCGATAACGGAGATGGAAATA 609
QY 815 GTGAGTGAACAGGGAGCAAGAGAAACAGAACCGACAGCTGTGTGTTATCCGTATGTC 874
DB 610 CTGAATGCAAAAGGGATGAAGGGGAACAGAGGGGACGGCGTGTACTCTCATCCCTTATC 669
QY 875 ACTTACTCATTTGTAATCAAGCGCTGCTCTTTTATACCTGTTCTCTTATATATACC 934
DB 670 ACGTATCTCTGCTGAGAGCGCTGCTTTTATCTATACCTCTTTCTCATATCCCTCC 729
QY 935 TGTAATGGGCTCTCAATTTTAACTGACTTACTTGTCTTCTATCTTCTTCAATGAAGTGAA 994
DB 730 TGCTGGGGCTGCTCTTCTTCAACAGTCTTGTGTTCTATTTACCTTCGATGAGGAGAA 789
QY 995 AAGATTGCTCTGCACTTCAGTACTTGTGCTTTTGAATGCTGCTTCTCTGTTATTTAA 1054
DB 790 AAACCTTCATTATCCACATCGCTCTGTGTTCTCTGACAGTTTTCCTTTTATGATTGAA 849
QY 1055 GAGATATACCATCATCTTCAAAAGTCATACCTTAATTTGGAGTACTTGGTATTTACC 1114
DB 850 GAAATCATCCCATCTCTTCAAAAGTCATCTCTCATTTGGAGAGTACTGCTGTTCATC 909
QY 1115 ATGATTTTGTGACACTGTCAATTATGTAACCGTCTTCGCTATCAACATTCATCATCGT 1174

DB 910 ATGATTTTGTGACCCCTGTCCATCATTTGTATACCGTGTGTGTCATTAACGTTTCAACACAGA 969
QY 1175 TCTTCTTCAACACACATAATGCCATGGCGCTTTGGTCCGCAAGATATTTCTTTCACACGCTT 1234
DB 970 TCTTCTTCCAGTACCACCCCATGGCCCTGGGTAAAGGCTCTTTCTGCAGNAACTT 1029
QY 1235 CCCAACTGCTTTGCATGAGAAAGTCATGTAGACAGGTAAT 1274
DB 1030 CCAAAATTTACTTTGTCATGAAAGATCATGTGGATCGTACTCATCCCAAGAAAGAGGAG 1089
QY 1275 -----TCACTCAGAAAGAGGAACTGAGAGTGGTAGT 1306
DB 1090 AGTCAACACAGTAGTGAAGGCAAAAGTCTCGAAAAAAGAAACAGAAACAGCTTAGTGAT 1149
QY 1307 GGACCAAAATCTTCTAGAAACACATTCGAACTCGCTCAATTTCTATTTCGCTACATTACA 1366
DB 1150 GGAGAAAAGTCTAGTTGCTTTTGGAAAAGCTGCTGATTCATTTAGATACATTTGG 1209
QY 1367 AGACACATCATGAAGGAAATGATGTCGAGGTTGTTGAAGATTTGAAATTCATAGCC 1426
DB 1210 AGACATGTGAAGAAAGAACATTTTATCAGCCAGGTAGTACAAGACTGGAAATTTGTAGCT 1269
QY 1427 CAGGTTCTTGTATCGATGTTTCTGTCGACTTTTCTTTTCTTTTCAATTTGTTGGATCTTT 1486
DB 1270 CAACTTCTTGACCGAAATCTTCTGTCGCTCTTCTGATGTCAGTAAACAGGCTCGGTT 1329
QY 1487 GGGCTTTTGTCTGTTTATTATATAAATGGCAATA 1523
DB 1330 CTGATTTTACCCCTGCTTTGAAGATGGCTACATA 1366

RESULT 6
ABV73250
ID ABV73250 standard; cDNA; 1927 BP.
XX
AC ABV73250;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human neuronal NACHR beta3 subunit encoding cDNA.
XX
KW Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
KW immunochemistry; NACHR beta3 subunit; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 98..1474
FT /*tag= a
FT /product= "NACHR beta3 subunit"
FT /note= "neuronal nicotinic acetylcholine receptor"
XX
PN WO200259266-A2.
XX
PD 01-AUG-2002.
XX
PF 29-OCT-2001; 2001WO-US50985.
XX
PR 01-NOV-2000; 2000US-0703951.
XX
PA (MERI) MERCK & CO INC.
XX
PI Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
XX
DR WPI; 2002-698532/75.
DR P-PSDB; ABB82437.
XX
PT Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro
PT screening of a drug substance in a test system specific for humans
XX
PS Examples; Page 136-138; 143pp; English.

XX The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (nAChR). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal nAChR beta3 subunit
CC encoding cDNA.

XX SQ Sequence 1927 BP; 508 A; 455 C; 422 G; 542 T; 0 other;

Query Match 30.3%; Score 554.2; DB 24; Length 1927;
Best Local Similarity 66.2%; Pred. No. 1.8e-124;
Matches 858; Conservative 0; Mismatches 388; Indels 51; Gaps 2;

QY 278 TCATTGCAAAACATGAAGATGTTGCTTAAGATTATTTCAAGACTACGAAGATGG 337
DB 167 TCAATCGCCGAAATGAAGATGCCCTCCTCAGACATTTGTTCCAAAGTTATCAGAAATGG 226
QY 338 GTTCGTCTCTGTGGAACACCTGAAATGACAAAATAAAAAATAAAATTTGGACTTGCATATCT 397
DB 227 GTCCGCCCTGATTACATCTTATGACACCAATTAAGATATTTTGGATTGAATATCC 286
QY 398 CAATTTGGTGAATGGATGAGAAAATCAGTTAATGACAAACAAACGCTGTGGTTGAAACAG 457
DB 287 CAGCTTGTAGATGGATGAAAGAAATCAGCTGATGACAAACCAATGTGTGGCTCAAAACAG 346
QY 458 GAATGATGATGATAAATTAAGATGGAACCTGATGACTATGTTGGAATAAAAGTTATA 517
DB 347 GAATGGACAGACCAACAAAGTTACGCTGGAATCCTGATGATTATGGTGGATCCATTCATT 406
QY 518 CGTGTCTCTTCAGACTCTGTGACACCAAGATCGTTTGTGATATGACAGATGGA 577
DB 407 AAGTTCCATCAGAACTCTGTGGCTTCCTGACATAGTTCTTTGAAATGCTGACGGC 466
QY 578 CGTTTGAAGGACCAAGTACGAAACAGATC---AGGTACAAATGGCACTGTCACTGG 634
DB 467 CGCTTCGAAGGCTCCCTGATGACCAAGGTCTCGTGAATCAAAACGAACTGTGTCTGG 526
QY 635 ACTCCACGGCAACTACAAAGTTCTGTACCATGATGCTCAGCTTTTCCCATTTGAC 694
DB 527 ACCCTCCCGCAGCTACAAAAGCTCTGCACCATGGACGTCAGTTTTTCCGCTTCGAC 586
QY 695 CTTTCAGAACTGTTCCTGAAATTTGGTTCTGTGACTTATGATGATCAGAGTTGATATA 754
DB 587 CGACAGNACTGCTCCATGAAGTTGGATCTGTGACTTATGATGGCACCATGGTTGACCTC 646
QY 755 ATTCTAGAGGACCAAGATGTAGACAAGAGATTTTTTTGATAATGGAGATGGGAGATT 814
DB 647 ATTTTGATCAATGAAATGTCGACAGAAAAGACTTCTTTCGATAACGAGAAATGGGAAATA 706
QY 815 GTGAGTCAACAGGACCAAGGAAAGCAACGACGAGCTGTGTGGTATCCGTATGTC 874
DB 707 CTGAATGCAAGGGGATGAAGGGGGAACAGAAAGGACGGCGGTACTCTATCCCTTTATC 766
QY 875 ACTTACTCATTTGTAATCAAGCGCTGCCCTCTCTTTTATACCTTGTTCCTTATAATACCC 934
DB 767 ACGTATTCCTTCGCTGACAGCGCTGCTTATCTATACCTCTTTCTCATCATCCCC 826
QY 935 TGTATGGGCTCTCATTTTTTAAGTACTGTCTTCTATCTTCTTCAAAATGAAGGTGAA 994
DB 827 TGCCTGGGGCTGCTTTCTCCCTAAACAGTCTTGTGTCTTATTTACCTTCGGATGAAGGAA 886
QY 995 AAGATTGTCTCTGCACCTCAGTACTGTGTCTTTGACTGTCTTCTCTCTCTGGTTATGAA 1054
DB 887 AAACCTTTTCATTATCCACATCGGTCTGGGTTTCTCTGACAGTTTCTCTTTAGTATGAA 946

QY 1055 GAGATCATACCATCATCTTTCAAAGTCATACCTCTAAATTGGAGAGATCTGGTATTTACC 1114
DB 947 GAAATCATCCCATCGTCTTTCCAAAGTCATCTCTCATTTGGAGAGTACCTGTGTTTCATC 1006
QY 1115 ATGATTTTGTGACACTGTCAATTTATGGTAAACGGTCTTCGCTATCAACATTCATCATCGT 1174
DB 1007 ATGATTTTGTGACCTGTCCATCATTTGTTACCGTGTGTTGTTATTAACGTTTACCACAGA 1066
QY 1175 TCTTCTCTCAACACATAATGCCATGGCGCTTTGGTCCGCAAGATATTTCTTTCACACGCTT 1234
DB 1067 TCTTCTTCACGTACCAACCCATGGCCCTGGTTAAGAGGCTCTTTCTGAGAAACTT 1126
QY 1235 CCCAACTCTTTGATGATGAGAGTCAATGATGACAGGTACT----- 1274
DB 1127 CCAAAATTTACTTTTGCATGAAAGATCATGTGGATCGCTACTCTCCCAAGAAAGAGGAG 1186
QY 1275 -----TCATCTCAGAAAGAGAAACTCAGAGTGGTAGT 1306
DB 1187 AGTCAACCAAGTAGTGAAGGCAAGTCTTCGAAAGAAAGAAACAGAAACAGCTTAGTGAT 1246
QY 1307 GGACCAAAATCTTCTAGAAACACATTTGGAAGCTGGCTCAATTTCTATTCGCTACATACA 1366
DB 1247 GGAGAAAAGTTCTAGTGTCTTTTGGAAAAGCTGCTGATTCATTTAGATACATTTCC 1306
QY 1367 AGACACATCATGAAGGAAATGATGCTCGTAGGTTGTTGAAGATTTGGAATTCATAGCC 1426
DB 1307 AGACATGTGAAGAAAGAACATTTTATCAGCCAGGTAGTACAAGACTGGAAATTTGTAGCT 1366
QY 1427 CAGGTTCTTGATCGGATGTTCTGTGGACTTTCTTTTCGTTTCAATTTGTTGGATCTCTT 1486
DB 1367 CAAGTCTTTGACCGAATCTTCTGTGGCTCTTTCTGATAGTGTGACAAACAGGCTCGGT 1426
QY 1487 GGGCTTTTGTCTCTTATTTATAAATGGCAATA 1523
DB 1427 CTGATTTTACCCCTGCTTTGAAGATGTGGCTACATA 1463

RESULT 7

ABSS4877
ID ABSS4877 standard; cDNA; 1927 BP.

XX ABSS4877;

DT 06-DEC-2002 (first entry)

XX Human neuronal nicotinic acetylcholine receptor beta 3 subunit cDNA.

XX Human; neuronal nicotinic acetylcholine receptor; nAChR; gene; ss;
KW ion flux; beta 3 subunit.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 98..1474
FT /*tag= a
FT /product= "Human nAChR beta 3 subunit"

XX US6440681-B1.

XX 27-AUG-2002.

XX 07-JUN-1995; 95US-0487596.

XX 03-APR-1990; 90US-0504455.

XX 30-NOV-1992; 92US-0938154.

XX 08-MAR-1993; 93US-0028031.

XX 08-NOV-1993; 93US-0149503.

XX (MERI) MERCK & CO INC.

XX Elliott KJ, Ellis SB, Harpold MM;

XX WPI; 2002-711528/77.

278	QY	TCTATTCCAAAA	CATGAAGATAGTTTGCCTTAAGGATTATTTCAAGACTACGAAAGATGG	337
167	Db	TCAATCGCGAAAA	TGAAGATGCGCTCTCTCAGACATTTTGTTCGAAGGTTATCAGAAATGG	226
338	QY	GTTCGTCCTCTGGAAC	CACTGAATGACAAATAAATAAATAATTTGGACTTGCATATCT	397
227	Db	GTCCGCCCTGTATTAC	ATTCCTTAATGACCAATAAAGTATATTTTGGATTGAAAATATACC	286
398	QY	CAATTTGGTGTGATGTG	GATGAGAAAAATCAGTTAATGACAAACAAACGTCGTGGTTGAAACAG	457
287	Db	CAGCTTGTAGATGTG	GATGAAGAATCAGCTGATGACCAACAATGTGTGCTCAACAG	346
458	QY	GAATGGATAGATGTAA	AATTAAAGATGAAACCTCGATGACTATGTGGAAATAAAAGTTATA	517
347	Db	GAATGGACACACACA	AGTTACGCTGGAATCCTCATGATTTATGTGGGATCCAATCCATT	406
518	QY	CGTGTTCCTTCAGACT	CTGTCTGACACACAGACATCGTTTTGTTTGTAATGCGATGGA	577
407	Db	AAAGTTCCATCAGAAT	CTCTGTGGCTTCCTGACATAGTTCTCTTTGAAAATGCTGACGGC	466
578	QY	CGTTTTGAAGGGAC	CCAGTACGAAAAACAGTCAATC---AGGTACAATGGCACTGTCACTGG	634
467	Db	CGCTTCGAAGGCTCC	CTGATGACCAAGTCACTGTGAATCAACCGGAACCTGTGTCTCG	526
635	QY	ACTCCACCGGCAAA	ACTACAAAGTTCCTGTACCATAGATGTCAGCTTTTCCCACTTTGCAC	694
527	Db	ACCCCTCCCGCAGCT	ACAAAGCTCTGACCAATGGACGTCACGTTTTCCCGTTTCGAC	586
695	QY	CTTCAGAACTGTGTT	CCATGAAATTTGGTTCTTGGACTTATGATGATCAACAGTTGATATA	754
587	Db	CGACAGAACTGCTCC	ATGAAAGTTTGGATCCTGGACTTATGATGCAACCATGTTGACCTC	646
755	QY	ATTCTAGAGACCAAG	TGTAGACAGAGAGATTTTTTGTGAATATGGAGATGGAGATT	814
647	Db	ATTTTGATCAATGAAA	ATGTGACAGAAAAGACTTCTTCGATACGGAGAAATGGGAATA	706
815	QY	GTGAGTGAACAGG	GACAAAGGAAACAGAACCGACAGCTGTCTGCTGTATCCGTTATGTC	874
707	Db	CTGAATGCAAGGG	EATGAAGGGNAACAGAAAGGACCGGTGTACTCTCTATCCCTTTATC	766
875	QY	ACTTACTCATTTGT	TAATCAACGCGCTGCCTCTCTTTTATACCTTGTCTTATTAATACCC	934
767	Db	ACGTATTCTCTG	TCCTGAGACGCTGCCTTTATTCTATACCTCTTCTCATCATCCCC	826
935	QY	TGTTATGGGCTC	ATTTTTTAACGTACTGTCTTCTATCTTCTTCAAAATGAAGGTGAA	994
827	Db	TGCTCGGGCTGTCT	TTTCTTAAACAGTCTTGTGTCTTATTACCTTTCGATGAAGGAGA	886

Qy	995	AGATTGTCTCTGCACTTCAGTACTGTGTGCTTTGACGTGTCTTCTCTGTGGTTATTGAA	1054
Db	887	AAATCTTCATTAATCCACATCGGCTTTGGTTTCTCTGACAGTTTTTCTTTTAGTGATTGAA	946
Qy	1055	GAGATCATACCATCATCTCTTCAAAGTCATACCTCTAAATGGAGAGTATCTGGTATTATTACC	1114
Db	947	GAATCATCCATCGTCTTCCAAAGTCATCTCTCATTTGGAGAGTACCTGCTGTTTCATC	1006
Qy	1115	ATGATTTTGTGACACGTGCAATTAATGGTAACCGTCTTCGCTATCAACATTCATCATCGT	1174
Db	1007	ATGATTTTGTGACCCCTGTCCATCAATGTTACCGTGTGTTGTCATTAAAGGTTCAACCACAGA	1066
Qy	1175	TCCTTCCTCAACACATATGCCATGGCGCCCTTTGGTCGCGAAGATATTCTTTCACACGCTT	1234
Db	1067	TCCTTCCTCCACGTACCAACCCCATGGCCCCCTGGGTTAAAGAGGCTCTTCTTCGCAGAAACTT	1126
Qy	1235	CCCAAACTGCTTTGGCATGAGAAGTCATGTAGACAGGTACT-----	1274
Db	1127	CCAAATTAATTCTTGGCATGGAAGTCAATGTGGATCGCTACTCTCCCGAGAGAAGAGGAG	1186
Qy	1275	-----TCACTCAGAAAGAGGAACTGAGAGTGGTGTGTTGAAGATTGGAAATTCATAGCC	1426
Db	1187	AGTCAACCACTAGTAGAAAGGCAAAAGTCCTCGAAAAAAGAAACAGAAACAGCTTAGTGAT	1246
Qy	1307	GGACCAAAATCTTCTAGAAACACATTTGGAGCTGCGCTCAATCTTATTTCCTACATTACA	1366
Db	1247	GGAGAAAAAGTCTTAGTGTCTTTTGGAAAAAGCTGCTGATTTCCATTAGATACATTTCC	1306
Qy	1367	AGACACATCATGAAGGAAATATGATGTCGCTGAGGTTGTTGAAGATTGGAAATTCATAGCC	1426
Db	1307	AGACATGTGAGAAAGAACATTTATCAGCCAGTAGTACAGACTGGAAATTTGTAGCT	1366
Qy	1427	CAGGTTCTGATCGGAGTTTCTGAGGACTTTTCTTTTCGTTTCAATGTTGGATCTCTT	1486
Db	1367	CAAGTTCTTGACCGAATCTTCTGTGGCTCTTCTCATAGTGTGAGCAACAGGCTCGGTT	1426
Qy	1487	GGGCTTTTGTTCCTGTTATTATTAATGGCAATA	1523
Db	1427	CTGATTTTACCCTCTTGAAGATGTGGCTACATA	1463
RESULT 8			
AAD20826			
ID	AAD20826 standard; DNA; 1638 BP.		
XX	AAD20826;		
XX	03-JAN-2002 (first entry)		
DE	Human CHRN3 partial gene containing exon 5 #1.		
XX	Human; cholinergic receptor, nicotinic, beta polypeptide 3; CHRN3;		
KW	single nucleotide polymorphism; SNP; drug screening; Alzheimer's disease;		
KW	neurological disorder; gene therapy; genotyping; haplotyping; ds.		
OS	Homo sapiens.		
XX	Key		
FH	variation		
FT	Location/Qualifiers		
FT	replace (268, A)		
FT	/*tag= a		
FT	/standard name= "Single nucleotide polymorphism"		
FT	variation		
FT	replace (318, A)		
FT	/*tag= b		
FT	/standard name= "Single nucleotide polymorphism"		
FT	exon		
FT	431..1313		
FT	/*tag= c		
FT	/number= 5		
XX	WO200175063-A2.		
PN	XX		
XX	11-OCT-2001.		
XX	XX		

11-OCT-2001.

PF 30-MAR-2001; 2001WO-US10277.
XX PR
XX 03-APR-2000; 2000US-194162P.
XX (GENA-) GENAISSANCE PHARM INC.
PA (CHEW/) CHEW A.
PA (CHOI/) CHOI J. Y.
PA (KOSH/) KOSHY B.
PA (STEP/) STEPHENS J. C.
XX PI
XX Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2001-626425/72.
XX
XX New polynucleotide, useful for studying expression and function of
PT CHRN3, comprises polymorphic variant of cholinergic receptor,
PT nicotinic, beta polypeptide 3 (CHRN3) gene, containing one of
PT polymorphic sites PS1-PS8 -
XX
XX Claim 19; Fig 5; 68pp; English.
XX
XX The invention relates to methods for haplotyping cholinergic receptor,
CC nicotinic, beta polypeptide 3 (CHRN3) gene. The invention also
CC provides single nucleotide polymorphisms (SNP) in the human CHRN3 gene.
CC Polymorphic variants of CHRN3 gene is used for screening for candidate
CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3
CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is human CHRN3
CC partial gene. Human CHRN3 gene includes 8 polymorphic sites PS1-PS8.
XX
SQ Sequence 1638 BP; 480 A; 354 C; 363 G; 441 T; 0 other;

Query Match 20.7%; Score 377.6; DB 22; Length 1638;
Best Local Similarity 71.6%; Pred. No. 1.4e-81;
Matches 510; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

QY 566 AATGACAGATGGAGTTTGAAGGACCAAGTACGAAACAGTCATC---AGGTACATGGC 622
DB 429 AGTGCTGACGCGCGCTCGAAGGCTCCCTGATGACCAAGGTCATCGTGAATCAACGGA 488
QY 623 ACTGTCACCTGGACTCCACCGGCAAACTACAAAGTTCCTGTACCATAGATGTCACGTTT 682
DB 489 ACTGTTGCTGGACCCCTCCCGCAGCTACAAAGTCTCCGACCATGGACGTCACGTTT 548
QY 683 TTCCCATTTGACCTTCAGAACTGTTCATGAAATTTGGTTCTTGGACTTATGATGATCA 742
DB 549 TTCCCGTTCCGACGACAGAACTGCTCCATGAAGTTTGGATCTTGGACTTATGATGACCC 608
QY 743 CAGGTTGATATAATTTAGAGGACCAAGATGTAGACAAAGAGAGATTTTTTGTATATGGA 802
DB 609 ATGGTTGACCTCATTTTGTATCAATGAAATGTGCACAGAAAGAACTTCTTCGATAACGGA 668
QY 803 GAATGGAGATTTGAGTGCACAGGAGCAAGGAAACAGACCCGACAGCTGTGCTGG 862
DB 669 GAATGGAAATGACTGAATGAAAGGGATGAAGGGGAAACAGAGGGCGGCTGTACTCC 728
QY 863 TATCCGTTATGCTACTTACTTATGTAATCAAGCGCTGCTCTCTTTTATACCTTTTC 922
DB 729 TATCCCTTTATCAGTATCTCTGCTCTGAGAGCGCTGCTTTATTTATACCTCTTT 788
QY 923 CTATATAATACCTGTATGGGCTCTCATTTTAACTGATCTGTGCTTCTATCTTCCTCA 982
DB 789 CTATCATCCCTGCTGGGCTGCTCTTCTTCAACAGTCTTGTGTTCTATTTACCTTCG 848
QY 983 AATGAGGTGAAAGATTTGCTCTGACATCTGATCTGCTGCTTTGACTGTCTTCCTT 1042
DB 849 GATGAGGAGGAAAAAATCTTATTCACATCGGCTGTGGTTCTCTGACAGTTTTCCTT 908
QY 1043 CTGTTTATTGAAGAGATCATACCATCATCTTCAAAAGTCATACCTCTTAATTGGAGAGTAT 1102

DB 909 TTAGTGATTGAAGAAATCATCCATCGTCTTCCAAAGTCATTCTCTCATTTGGAGATAC 968
QY 1103 CTGGTATTTACCATGATTTTGTGACACTGTCAATTTATGTAACCGCTTTCGCTATCAAC 1162
DB 969 CTGCTGTTTCATCAAGATTTTGTGACCCCTGTCCATCATTTGTTACCGTGTGTTGTCATTAAC 1028
QY 1163 ATTATCATCATGTTCTTCTCAACACATAATGCCATGGCGCTTTGGTCGCAAGATATTT 1222
DB 1029 GTTCACCCAGAGATCTTCTTCCACGTACACCCCATGGCCCTGGGTAAAGAGGCTCTTT 1088
QY 1223 CTTACACAGCTTCCAAACTGCTTTGCATGAGAGTCATGTAGACAGGTACT 1274
DB 1089 CTGCAGAAACTTCCAAATTTACTTTTGCATGAAAGATCATGTGGATCGCTACT 1140

RESULT 9
AAD20870
ID AAD20870 standard; DNA; 1638 BP.
XX
XX AAD20870;
XX
XX 03-JAN-2002 (first entry)
XX
XX Human CHRN3 partial gene containing exon 5 #2.
XX
XX Human; cholinergic receptor, nicotinic, beta polypeptide 3; CHRN3;
XX single nucleotide polymorphism; SNP; drug screening; Alzheimer's disease;
XX neurological disorder; gene therapy; genotyping; haplotyping; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT misc_feature 253
FT /tag= a
FT /note= "This degenerate base represents polymorphic
FT site PS7"
FT misc_feature 268
FT /tag= b
FT /note= "This degenerate base represents polymorphic
FT site PS6"
XX
XX WO200175063-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10277.
XX
XX 03-APR-2000; 2000US-194162P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX (CHEW/) CHEW A.
XX (CHOI/) CHOI J. Y.
XX (KOSH/) KOSHY B.
XX (STEP/) STEPHENS J. C.
XX
XX Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2001-626425/72.
XX
XX New polynucleotide, useful for studying expression and function of
PT CHRN3, comprises polymorphic variant of cholinergic receptor,
PT nicotinic, beta polypeptide 3 (CHRN3) gene, containing one of
PT polymorphic sites PS1-PS8 -
XX
XX Disclosure; Page 67; 68pp; English.
XX
XX The invention relates to methods for haplotyping cholinergic receptor,
CC nicotinic, beta polypeptide 3 (CHRN3) gene. The invention also
CC provides single nucleotide polymorphisms (SNP) in the human CHRN3 gene.
CC Polymorphic variants of CHRN3 gene is used for screening for candidate
CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3

QY 592 ---CAGTACGAAACAGTCATCAGGTACATGCGACTGTGACCTGACCTCCACCGGCAA 648
 Db 639 CCATGATGACCAAGCCGACCTCTTCCAGCGGCACTGTGCACTGGTGGCCCGCCCAT 698
 QY 649 CTACAAAGTTCTGTACCATAGATGTGAGTTTCCCATTTGACCTTCAGAACTGTTTC 708
 Db 699 CTACAAAGTCTGTGAGCATGACGTGACCTTCTCCCTTCGACGAGCAAGTGCATA 758
 QY 709 CATGAAATTTGGTCTTGGACTTATGATGGATCACAGGTTGATATTAATCTAGAGGACCA 768
 Db 759 GATGAGTTTGGCTCTCGACTTATGACAAAGCCCAAGATCGACCTGGAGCAGATGGACA 818
 QY 769 AGATGTAGACAAGAGAGATTTTGTGATATGAGAGATGGAGATTTGTGAGTCAACAGG 828
 Db 819 GACTGTGGACCTGAAGACTACTTGGAGAGCGGAGTGGCCATCGTCAATGCCACGGG 878
 QY 829 GAGCAAGGAAACAGAACACAGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTC 882
 Db 879 CACCTTCAACAGCAAGAGTACGACTGCTGCGCGGAGATCTACCCGAGTCACTACGC 938
 QY 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATATACCTGTATTTG 942
 Db 939 CTTGTCATCCGGGCTGCGCTCTTACACCATCACTCATCCCTGCTGCT 998
 QY 943 GCTCTCAATTTTAACTGTACTGTCTTCTATCTTCTTCAATGAAGGTGAAAGATTTG 1002
 Db 999 CATCTCTGCTCACTGTGCTGCTTCTTACCTGCGCTCGACTGCGGCGAGAGATCAC 1058
 QY 1003 TCCTGCACTTCAAGTCTGCTGCTTGTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 1062
 Db 1059 GCTGTGATTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
 QY 1063 ACCATCATCTTCAAAAGTCAATCTCTAATTTGGAGAGTATCTGATTTTACCATGATTTT 1122
 Db 1119 CCGTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
 QY 1123 TGTGACATGTCATTAATGATGACCGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
 Db 1179 CGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1238
 QY 1183 AACACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
 Db 1239 CACCCACA---CCATGCCCACTGCGGTGCGGGGGGCGCTTCTGGGCTGTGTCGCCGGTG 1295
 QY 1243 GCTTTGCTATGA 1253
 Db 1296 GCTTCTGATGA 1306

RESULT 11
 ID AAQ90387 standard; cDNA; 2277 BP.
 AC AAQ90387;
 DT 25-MAR-2003 (updated)
 DT 30-NOV-1995 (first entry)
 DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
 KW Human nNACHr; neuronal nicotinic acetylcholine receptor;
 KW neurotransmitter; ss.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 166..1755
 FT /*tag= a
 XX WO9513299-A1.
 XX 18-MAY-1995.
 XX

PF 08-NOV-1994; 94WO-US12859.
 PR 08-NOV-1993; 93US-0149503.
 XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 PA Elliott KJ, Ellis SB, Harpold WM;
 PI WPI; 1995-194036/25.
 DR P-PSDB; AAR73966.
 XX New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA
 PT used to develop prods. for detection, diagnosis and therapy and for
 PT modulating activity
 XX Claim 2; Page 43-46; 54pp; English.
 PS DNA encoding the human nNACHr alpha2 subunit was isolated from
 CC human thalamus tissue cDNA library using corresp. rat cDNA. The
 CC insert of one clone obt. was ligated with the insert of another
 CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
 CC used to identify function nNACHrs. Cells contg. the DNA can be used
 CC for screening to identify cpds. which modulate the activity of human
 CC nNACHrs. The human nNACHr alpha 2 subunit can be used to product
 CC antibodies which can be used in immunohistochemistry, diagnosis and
 CC therapy. The nucleic acids can be used for analysing disease states
 CC and creating animal models.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 2277 BP; 451 A; 696 C; 643 G; 487 T; 0 other;
 SQ Query Match 18.3%; Score 334.6; DB 16; Length 2277;
 Best Local Similarity 61.3%; Pred. No. 4.7e-71;
 Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
 QY 292 TGAAGTATGTTGCTTAAGGATTATTTCAAGACTAGCAAGATGGTTGCTCTCTGGA 351
 Db 339 TGAGGACCGGCTCTTCAAAACACCTCTTCGGGGCTACAAACCGCTGGCGCGCCCGTGC 398
 QY 352 ACACCTGATGACAAATAAATAAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
 Db 399 CAACACTTCAGAGCTGGTGTATTTGGCTTTGGACTGTCCATCGCTCATCATGT 458
 QY 412 GGATGAGAAAAATCAGTTAATGACAAACAGTCTGGTTGAAACAGGAATGATAGATGT 471
 Db 459 GGATGAGAAAGAACAAATGATGACCAACAGTCTGGCTTAAACAGAGAGTGAGCGACTA 518
 QY 472 AAATTAAGATGGAACCTGATGACTATGTTGGATTAAGATTAATACGTGTTCTTCAGA 531
 Db 519 CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578
 QY 532 CTCTGTCTGGACACAGACATCGTTTGTGATATGAGATGAGACGTTTGAAGGAC 591
 Db 579 GATGATCTGGATCCCGACATTTGTTCTTACACATGAGATGGGAGTTGCACTGAC 638
 QY 592 ---CAGTACGAAACAGTCAATGAGTACATGCGACTGTGACCTGACCTCCACCGGCAA 648
 Db 639 CCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGGTGGCCCGCCAT 698
 QY 649 CTACAAAGTCTGTACCATAGATGTGACGTTTTCCTCCATTTGACCTTCAGCACTGTTTC 708
 Db 699 CTACAAAGTCTGTGAGCATGACCTTCTTCCCTTCGACGAGCAAGTGCATA 758
 QY 709 CATGAAATTTGGTCTTGGACTTATGATGGATCACAGGTTGATATTAATCTAGAGGACCA 768
 Db 759 GATGAGTTTGGCTCTCTGACTTATGACAAAGCCCAAGATCGACCTGGAGCAGATGGACA 818
 QY 769 AGATGTAGACAAGAGAGATTTTGTGATATGAGAGATGGAGATTTGTGAGTCAACAGG 828
 Db 819 GACTGTGGACCTGAAGACTACTTGGAGAGCGGAGTGGCCATCGTCAATGCCACGGG 878
 QY 829 GAGCAAGGAAACAGAACACAGCAGCTGTTGC-----TGGTATCCGTATGTCACTTACTC 882


```

1119 CCCTGACCTCGCTGCTATCCGCTCATCGCGAGTACCTGCTGTACCAATGATCTT 1178
1123 TGTGACACTGCTCAATATGTAACCGCTCTTCGCTATCAACATTCATCATGTTCTTCCTC 1182
1179 CGTCACCTGCTCATGCTATCACCGCTCTTCGCTCAATGTCGACACCGCTCCCGCAG 1238
1183 AACACATAATGCCATGCGCTTTGGTCCGCAAGATATTTCTTACACGCTTCCCAACT 1242
1239 CACCCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG 1295
1243 GCTTTGCATGA 1253
1296 GCTTCTGATGA 1306

```

RESULT 13

ABS54870 standard; cDNA; 2277 BP.

AC ABS54870;

06-DEC-2002 (first entry)

Human neuronal nicotinic acetylcholine receptor alpha 2 subunit cDNA.

Human; neuronal nicotinic acetylcholine receptor; nNACHr; gene; ss;
ion flux; alpha 2 subunit.

OS Homo sapiens.

Key Location/Qualifiers

CDS 166..1755

/tag= a

/product= "Human nNACHr alpha 2 subunit"

US6440681-B1.

27-AUG-2002.

07-JUN-1995; 95US-0487596.

03-APR-1990; 90US-0504455.

30-NOV-1992; 92US-0938154.

08-MAR-1993; 93US-0028031.

08-NOV-1993; 93US-0149503.

(MERI) MERCK & CO INC.

Elliot KJ, Ellis SB, Harpold MM;

WPI; 2002-711528/77.

P-PSDB; ABG31800.

Identifying antagonists or agonists of human neuronal nicotinic
acetylcholine receptors, by contacting recombinant cells with test
compound, and measuring ion flux of cells or binding of compound to
nNACHr -

Claim 1; Column 29-32; 56pp; English.

The invention relates to a method for identifying compounds that are
antagonists or agonists of human neuronal nicotinic acetylcholine
receptors (nNACHrs), by contacting recombinant cells with a test
compound and measuring ion flux, the electrophysiological response of the
cells or binding of the test compound to the nNACHr. The recombinant
cells are produced by transfection with a nucleic acid encoding at least
one human nNACHr (alpha or beta) subunit, such that the cells express an
nNACHr comprising one human subunit encoded by the transfected nucleic
acid. This sequence represents cDNA encoding the alpha 2 subunit of the
human nNACHr polypeptide.

Sequence 2277 BP; 451 A; 695 C; 643 G; 486 T; 2 other;

Query Match	18.3%;	Score 334.6;	DB 24;	Length 2277;
Best Local Similarity	61.3%;	Pred. No. 4.7e-71;		
Matches 595;	Conservative	0;	Mismatches 364;	Indels 12;
Gaps	3;			

QY	292	TGAGATAGTTGCTTAAGGATTTATTTCAAGACTACGAAAGATGGTTGCTCTCTGGA	351
DB	339	TGAGGACCGGCTCTTCAAAACACCTCTTCGGGGCTACAAACCGCTGGCGCGCCCGTGCC	398
QY	352	ACAACCTGAATGACAAAATAAAATTTGGACTTGCATATCTCAATATGGTGTGATGT	411
DB	399	CAACACTTCAGACGGTGTGTTGGCTTTGGACTGTCCATCGCTCAGCTCATCATGT	458
QY	412	GGATGAGAAAAATCAAGTTAATGACAAACACCTCTGGTTGAAACAGGAATGAGATAGT	471
DB	459	GGATGAGAAAGAACCAAAATGATGACCAACACCTCTGGCTTAAACAGGAGTGGAGCGACTA	518
QY	472	AAATTAAGATGGNAACCTGATGACTATGTTGGATATAAAGTTATACGTGTTCTTCA	531
DB	519	CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA	578
QY	532	CTCTGCTGACACACAGACATCGTTTGTGATATGAGATGAGACGTTTGAAGGGAC	591
DB	579	GATGATCTGATCCCGACATTTGTTCTTCAACAATGAGATGGGAGTTTGCATGAC	638
QY	592	---CAGTACGAAAAACAGTATCAGGTACAAATGGCACTGTCACTGACCTCCACCGCAAA	648
DB	639	CCACATGACCAAGGCCACCTCTCTCCACGGGCACTGTGCATCTGGGTGCCCGGCCAT	698
QY	649	CTACAAAAGTTCTGTACCATAGATGTCAGTTTTCCTTCCATTTGACCTTCAGACACTTTC	708
DB	699	CTACAAGAGCTCTGTCAGCATGACGTCACTTCTTCCCTTCGACACGAGAACTGCAA	758
QY	709	CATGAATTTGTTCTTGGACTTATGATGGATCACAGGTTGATATAATTTCTAGAGACCA	768
DB	759	GATGAAGTTTGGCTCTGACCTTATGACAAGGCCAAGATCGACCTGGAGCAGATGAGCA	818
QY	769	AGATGTAGACAAGAGAGATTTTGTGATATGGAGATGGGAGATTTGAGTGCAACAGG	828
DB	819	GACTGTGGACCTGAAGGACTACTTGGGAGAGCGGAGTGGCCATCGTCAATGCCACGGG	878
QY	829	GAGCAAGGAACAGNACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTAC	882
DB	879	CACCTACAACAGCAAGATGACGACTGTGCGCGGAGATCTACCCGCGAGCTCACCTACGC	938
QY	883	ATTGTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATATACTCTGTTATGG	942
DB	939	CTTGTGTCATCCGGCGCTGCGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCT	998
QY	943	GCTCTCAATTTTAACCTGTACTTGTCTTCTTCTTCTTCTTCAAAATGAAGGTGAAGATTTG	1002
DB	999	CATCTCTGCTCAGTGTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1058
QY	1003	TCTGTCACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1062
DB	1059	GCTGTGATTTTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	1118
QY	1063	ACCATCATCTTCAAAAAGTCATACCTCTAATTTGGAGAGTATCTGGTATTTTACCATGATTT	1122
DB	1119	CCGTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1178
QY	1123	TGTGACACTGTCAATTTATGTTAAACCGTCTTGGCTATCAACATTCATCATCTTCTTCTC	1182
DB	1179	CGTCACCTGTCCATCGTCAACCGTCTTGGTCTCAATGTGTCACACCGCTCCCGCAG	1238
QY	1183	AACACATAATGCGATGGCGCTTGTGTCGCAAGATATTTCTTCAACAGCTTCCCAACT	1242
DB	1239	CACCCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG	1295
QY	1243	GCTTTGCATGA 1253	
DB	1296	GCTTCTGATGA 1306	

RESULT 14
 AAT48235
 ID AAT48235 standard; DNA; 2664 BP.
 XX
 AC AAT48235;
 DT 09-APR-1997 (first entry)
 DE Neuronal nicotinic acetylcholine receptor alpha-2 subunit DNA.
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor; ds.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 555..2141
 FT /*tag= a
 XX
 PN WO9641876-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09775.
 XX
 PR 07-JUN-1995; 95US-0484722.
 XX
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Elliott KJ, Harpold MM;
 XX
 DR WPI; 1997-065463/06.
 DR P-PSDB; AAW09021.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 XX
 PS Disclosure; Page 49-52; 108pp; English.
 XX
 CC A DNA sequence (AAT48235) codes for the alpha-2 subunit (AAW09021) of
 CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host
 CC cells, esp. mammalian cells or amphibian oocytes, carrying alpha-2
 CC nucleic acids, opt. in combination with other alpha and/or beta
 CC subunit nucleic acids (see also AAT48232-34, AAT48236-41), express
 CC recombinant nAChR subunits useful for identifying cpds. that
 CC modulate the activity of human nAChRs.
 XX
 SQ Sequence 2664 BP; 518 A; 815 C; 743 G; 588 T; 0 other;
 Query Match 18.3%; Score 334.6; DB 18; Length 2664;
 Best Local Similarity 61.3%; Pred. No. 5, 1e-71;
 Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
 QY 292 TGAAGATGTTGCTTAAGATTTATTCAGACTACGAAAGATGGTTCGCTGTGGA 351
 DB 728 TGAGGACCGGCTCTTCAACACCTCTCCGGGGCTACAACCGCTGGCGCGCGGTC 787
 QY 352 ACACCTGATGACAAATTAATAATTTGGACTTGCATATCTCAATTGGTGATGT 411
 DB 788 CAACACTTCAGACGGTGGTGAATTTGGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 847
 QY 412 GGATGAGAAAATCAGTTAATGACAAACAACTCTGGTTGAAACAGGAATGATAGATGT 471
 DB 848 GGATGAGAGAACCAATGATGACCAACCACTCTGGCTTAACAGGAGTGAGCGACTA 907
 QY 472 AAAATTAAGATGAAACCCCTGATGACTATGGTGAATAAAGTTATACGTTTCCTTCAGA 531
 DB 908 CAAACTGCGCTGGAACCCCGCTGATTTGGCAACATCATCTCTCAGGTCCTTCTGA 967
 QY 532 CTCTGCTGGACACAGACATCGTTTGTGTTGATTAATGAGATGACGTTTGAAGGAC 591
 DB 968 GATGATCTGGATCCCCGACATTTGTTCTCTACAAACATGAGATGGGAGTTTGCAGTGAC 1027

QY 592 ---CAGTACGAAAAACAGTCATCAGGTACAAATGGCACTGTCTCACTGGACTCCACCGGCAAA 648
 DB 1028 CCACATGACCAAGCCACACCTCTTCTCAAGGCACTGTGCACTGGTGGCCCGCCAT 1087
 QY 649 CTACAAAAGTTCCCTGTACCATAGATGTCAGCTTTTCCCATTTGACCTTCAAGACTGTTC 708
 DB 1088 CTACAAGAGCTCTCTGCAGCATCGACGTCACCTTCTCCCTTCGACCGAGAACTGCAA 1147
 QY 709 CATGAAATTTGGTTCTTTGGACTTATGATGGATCACAGTTGATATAATTTCTAGAGGACCA 768
 DB 1148 GATGAGTTTGGCTCTTGGACTTATGACAAGGCCAAGATCGACCTGGAGCAGATGGAGCA 1207
 QY 769 AGATGTAGACAAGAGAGATTTTTTGTATAATGGAGAATGGGAGATTTGTAGTGCACAAGG 828
 DB 1208 GACTGTGGACCTGAAGGACTACTGGGAGAGCGGAGTGGGCCATCGTCAATGCCACGG 1267
 QY 829 GAGCAAGGAAACAGAACCGACAGCTGTTC-----TGGTATCGGTATGTCACTTACTC 882
 DB 1268 CACCTACAAACAGCAAGATACGACTGTGCGCGGAGATCTACCCCGACGTCACCTAGCG 1327
 QY 883 ATTTGTAATCAAGCGCTCGCTCTCTTTTATACCTTGTTCCTTATAATACCTGTATTGG 942
 DB 1328 CTTGTCATCCGCGGCTCGCGCTCTTCTACACCATCAACCTCATATCCCTCGCTGCT 1387
 QY 943 GCTCTCATTTTTAACTGTACTTGTCTTCTATCTTCTTCTTCAAAATGAAGGTGAAAAGATTG 1002
 DB 1388 CATCTCGCTCACTGTGCTGGTCTTCTTACTCGCTCCGACTCGGCGGAGAGATCAC 1447
 QY 1003 TCTCTGCACTTCAGTACTTGTGTCTTTGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1062
 DB 1448 GCTGTGCAATTCGGTGTCTGTCTCACTCAGCGTCTTCTGCTGTCTCATCTGAGATCAT 1507
 QY 1063 ACCATCATCTTCAAAAGTCATACCTCTAATTTGGAGAGTATCTGTATTTTACCATGATTTT 1122
 DB 1508 CCGTCCACCTCGCTGTGTCATCCGCTCATCGGAGTACTGTCTGTCTCACCATGATCTT 1567
 QY 1123 TGTACACTGTCAATTTATGTTAAACCGTCTTCGCTTATCAACATTCATCATGCTTCTTCTC 1182
 DB 1568 CGTCACCTGTCCATCGTCATCACCGTCTTCGTCATGTCACACCGCTCCCGCAG 1627
 QY 1183 AACCATTAATGCAATGGCGCTTTGGTTCGCAAGATATTTCTTCAACAGCTTCCCAACT 1242
 DB 1628 CACCCACA---CCATGCCCACTGGGTGGCGGGGGCCCTTCTTGGGCTGTGTGCCCCGGTG 1684
 QY 1243 GCTTTGCATGA 1253
 DB 1685 GCTTCTGATGA 1695
 RESULT 15
 ABK92165
 ID ABR92165 standard; DNA; 2664 BP.
 XX
 AC ABK92165;
 DT 15-AUG-2002 (first entry)
 DE Prostate cancer-associated DNA sequence #51.
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 OS Mammalia.
 XX
 PN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.

PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
XX P-PSDB; ABG61850.
XX Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue -
XX Claim 22; Page 338; 436pp; English.
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridize to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.
XX
SQ Sequence 2664 BP; 518 A; 815 C; 743 G; 588 T; 0 other;
Query Match 18.3%; Score 334.6; DB 24; Length 2664;
Best Local Similarity 61.3%; Pred. No. 5.1e-71;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATAGTTGCTTAAGGATTATTCAAGACTACGAAGATGGGTTCTGCTGTGGA 351
DB 728 TGAGGACCGGCTCTTCAACACCTCTTCGGGGCTACACCGCTGGGGCGCGCGTGCC 787
QY 352 ACACCTGAATGACAAATAAATAATTTGGACTTGGCAATCTCAATTTGGTGGATGT 411
DB 788 CAACACTTCAGACGTGGTGGATTTGGCGCTTTGGACTGTCCATCGCTCATCGATGT 847
QY 412 GGATGAGAAAATCAGTTAATGACAAACACGCTGGTTGAAACAGGAATGGATAGATGT 471
DB 848 GGATGAGAGAACCAATGATGACCAACAGCTGGCTTAACAGAGGTGGAGCGACTA 907
QY 472 AAAATTAAAGATGGAACCCCTGATGACTATGGTGGAAATAAAGTTATACGTTTCTTCAGA 531
DB 908 CAAACTCGCTGGAACCCCGCTGATTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA 967
QY 532 CTCTGTCTGGACACCAACATCGTTTGTGTTGTAATGAGAGATGGACGTTTGAAGGGAC 591
DB 968 GATGATCTGGATCCCGACATCTGTTCTCTACAAATGAGATGGGGAGTTTGCAGTGAC 1027
QY 592 ---CAGTACGAAACAGTCATCAGGTACATGGCAGCTCACCTGGACTCCACCGGCAAA 648
DB 1028 CCACATGACCAAGGCCACCTCTTCTCAGGGGACATGTGCATGGGTGCCCGGCCAT 1087
QY 649 CTACAAAGTTCTGTGTAACCATAGATGTACGTTTTCCTCCATTTGACCTTCAGAACTGTT 708
|||||

DB 1088 CTACAAGAGCTCCTGCGAGCATCGAGCTCACCTTCTTCCCTTCGACCCAGCAGAACTGCAC 1147
QY 709 CATGAAATTTGGTTCTTTGGACTTATGATGGATCACAGGTTGATATAAATCTAGAGGACCA 768
DB 1148 GATGAAATTTGGTTCTTTGGACTTATGATGAGGCAAGATCGACCTGGAGCAGATGAGCA 1207
QY 769 AGATGTAGACAAGAGAGATTTTGTGATTAATGGAGAAATGGAGATTTGTGAGTGCACAGG 828
DB 1208 GACTGTGGACCTGAAGGACTACTGGGAGAGCGGAGTGGGCATCTCTCAATGCCACGGG 1267
QY 829 GAGCAAGGAAACAGAACCGACGAGCTGTTC-----TGGTATCCGTATGCTTACTTACTC 882
DB 1268 CACCTACAACAGCAAGATGACGACTGTGCGCGGAGATCTACCCCGAGCTCACCTACGC 1327
QY 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATATAATACCTGTATTTGG 942
DB 1328 CTTGTGATTCGGCGGCTGCGCTCTTCTACCATCAACCTCATCATCTCCCTGCTGCT 1387
QY 943 GCTCTCAATTTTAACTGTACTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1002
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QY 1003 TCTCTGCACTTCAGTACTTGTGCTTTGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1062
DB 1448 GCTGTGCAATTCGGTGTGCTGCTCACTCACCGCTTCTTCTTCTTCTTCTTCTTCTTCT 1507
QY 1063 ACCATCATCTTCAAAAGTCACTACCTTAATTTGAGAGATCTGGTATTTTACCATGATTTT 1122
DB 1508 CCGTCCACTCGTGGTGTATCCCGCTCATCGCGAGTACCTGCTGTTTCCCATGATCTT 1567
QY 1123 TGTGACACTGTCAATTTATGGTAAACCGCTTTCGCTATCAACATTCATTCGTTTCTTCT 1182
DB 1568 CGTCACTGTCCATCGTCTCATCACCGCTTCTTCTGCTCAATGTGCACACCGCTCCCCCAG 1627
QY 1183 AACACATAATGCCATGGCGCCTTTGGTCCGCAAGATATTTCTTTCACACGCTTCCCAACT 1242
DB 1628 CACCCACA---CCATGCCCCACTGGGTGGGGGGGCGCTTCTTGGGCTGTGTGCCCGCGTG 1684
QY 1243 GCTTTGCATGA 1253
DB 1685 GCTTCTGATGA 1695

Search completed: December 23, 2003, 18:47:17
Job time : 537 secs

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OM nucleic - nucleic search, using sw model
Run on: December 23, 2003, 15:35:43 ; Search time 6774 Seconds
(without alignments)
11039.681 Million cell updates/sec

Title: US-09-703-951A-7
Perfect score: 1828
Sequence: 1 CCGCGCGGAGCTGTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.ats.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1828	100.0	1828	6	AR224028	AR224028 Sequence
2	1828	100.0	1828	6	AR282831	AR282831 Sequence
3	1828	100.0	1828	6	AX658380	AX658380 Sequence
4	1828	100.0	1828	6	AX719084	AX719084 Sequence
5	1828	100.0	1828	9	HSU62434	U62434 Human nicot
6	1821.6	99.6	2468	9	BC033639	BC033639 Homo sapi
7	1642.6	89.9	1662	9	AF385586	AF385586 Homo sapi
8	1628.6	89.1	1679	9	AF385586	M83712 H. sapiens n
9	1405.4	76.9	1407	9	HSMACHRA5	Y08419 H. sapiens m
10	1212.2	66.3	1645	4	AF487464	AF487464 Bos tauru
11	1022.2	55.9	2895	10	RATNACHRR	J05231 Rat neurona
12	968.2	53.0	1445	10	AF204689	AF204689 Mus muscu
13	897.4	49.1	1365	5	CHKA5SUBU	J05642 Gallus dome
14	839.8	45.9	1526	9	HSK306485	AJ306485 Homo sapi
15	838.2	45.9	2194	9	BC050469	BC050469 Homo sapi
16	838.2	45.9	11700	9	AC067863	AC067863 Homo sapi
17	838.2	45.9	169377	9	AC027228	AC027228 Homo sapi
18	597.2	32.7	110000	2	AC110933	Continuation (4 of
19	597.2	32.7	23816	2	AC108616	AC108616 Rattus no
20	587.8	32.2	185429	2	AC122777	AC122777 Mus muscu
21	586.2	32.1	131604	2	AC108816	AC108816 Mus muscu
22	557.6	30.5	1924	9	HSU62438	U62438 Human nicot
23	557.6	30.5	1925	6	AR282835	AR282835 Sequence
24	557.6	30.5	1925	6	AX719092	AX719092 Sequence
25	556	30.4	1595	9	HSNACHR3B	Y08417 H. sapiens m
26	554.2	30.3	1927	6	AR224032	AR224032 Sequence
27	554.2	30.3	1927	6	AR257042	AR257042 Sequence
28	541.8	29.6	1439	9	HSNACHR3	Y08417 H. sapiens m
29	537.2	29.4	558	9	AF087690	X67513 H. sapiens m
30	521.4	28.5	1546	10	AF467896	AF467896 Mus muscu
31	513.6	28.1	2280	5	CGNACHR3	X83739 G.gallus mR
32	510.4	27.9	1389	5	AB087185	AB087185 Danio rer
33	509.8	27.9	2644	10	RATNACHR	J04636 Rattus norv
34	504	27.6	1789	5	CAACHR	X14786 Goldfish mR
35	485.8	26.6	505	5	MMU245974	AJ245974 Macaca mu
36	479.6	26.2	2163	5	AY256909	AY256909 Danio rer
37	470	25.7	2688	5	CRAGFNA3	M29529 Goldfish (C
38	377.6	20.7	1638	9	HSCNRNB5	AF140764 Homo sapi
39	376	20.6	44285	9	AC103843	AC103843 Homo sapi
40	376	20.6	150647	2	AF311104	AF311104 Homo sapi
41	376	20.6	154179	9	AC087533	AC087533 Homo sapi
42	363.2	19.9	176961	5	AL928917	AL928917 Zebrafish
43	353	19.3	245121	2	AC126482	AC126482 Rattus no
44	351.6	19.2	221259	2	AC102544	AC102544 Mus muscu
45	346.8	19.0	71864	2	AC103852	AC103852 Homo sapi

ALIGNMENTS

RESULT 1
AR224028 LOCUS AR224028 1828 bp mRNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6440681.
ACCESSION AR224028
VERSION AR224028.1 GI:23332636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1828)
AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.
TITLE Methods for identifying agonists and antagonists for human neuronal
nicotinic acetylcholine receptors
JOURNAL Patent: US 6440681-A 7 27-AUG-2002;

AUTHORS Elliott, K.J. and Harpold, M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and methods employing same
JOURNAL Patent: US 5524789-A 7 25-FEB-2003;
FEATURES Location/Qualifiers
 source 1..1828
 /organism="unknown"
BASE COUNT 496 a 372 c 419 g 541 t
ORIGIN
 Query Match 100.0%; Score 1828; DB 6; Length 1828;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 GCGGCTCCCGCGCTCCCGCGGCGGGCGGCGATGCGCGCGGGGTCAGGCGCCCG 180

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 Db 181 CGCGCTCCCGCTGCTGCTTTGGTCCAGCTGGTCCGGGGCGCTCGCGTCTAGCGGGCGC 240

 Qy 241 GCGGGCGGCGCGCAGAGAGATTATCTGAACCTTCTTATTCGAAAACATGAAGATAG 300
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 Qy 301 TTTGCTTAAAGATTATTTCAAGACTACGAAGATGGTTCGTCTGTGGACACCTGAA 360
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 Qy 361 TGCAAAATAAAATAAAATTGGACTTTGCAATATCTCAATTGGTGGATGGATGAGAA 420
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 Qy 421 AATCAGTTAATGACAAACAAACGCTCGTTTGAAACAGGAATGGATGATGTAATAAAG 480
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 Qy 481 ATGGAAACCTTGATGACTATGGTGAATAAAGTTATACGTGTTCCCTTCAGACTCTGCTG 540
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 Qy 541 GACACACAGACATCGTTTTGTTTGATATGACAGATGGAGCTTTTCAAGGGACACGATACGAA 600
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 Qy 601 AACAGTCATCAGGTACAAATGSCACTGTCACTGGACTCCACCGGCAAACTACAAAAGTTC 660
 Db 601 AACAGTCATCAGGTACAAATGSCACTGTCACTGGACTCCACCGGCAAACTACAAAAGTTC 660

 Qy 661 CTGTACCATAGATGTACGTTTTTCCATTTGACCTTCAGAACTGTGTCATGAAATTTGG 720
 Db 661 CTGTACCATAGATGTACGTTTTTCCATTTTCCATTTGACCTTCAGAACTGTGTCATGAAATTTGG 720

 Qy 721 TTCTTGACCTTATCATCGATCCACAGGTTGATATAATTTCTAGAGACCAAGATGTAGACAA 780
 Db 721 TTCTTGACCTTATCATCGATCCACAGGTTGATATAATTTCTAGAGACCAAGATGTAGACAA 780

 Qy 781 GAGAGATTTTTTTTGAATAATGGAGATTTGTGAGTGCAACACGGGAGCAAAAGGAAA 840
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 Qy 841 CAGAACCGACAGCTGTGCTGGTATCCGTATGTCACTTACTCATTTGTGTAATCAAGCGCT 900
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RESULT 4	AX719084	1828 bp	DNA	linear	PAT 15-APR-2003
LOCUS	Sequence 7 from Patent EP1295945.				
DEFINITION	AX719084				
ACCESSION	AX719084.1	GI:29891587			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 Elliott,K.J. and Harpold,M.M.				
JOURNAL	Human neuronal nicotinic acetylcholine receptor compositions and methods employing same				
FEATURES	Patent: EP 1295945-A 7 26-MAR-2003;				
source	MERCK & CO. INC. (US)				
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	155..1561				
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	EIVSGKSCNRTRDSCWPPYTYEIVIPSSKRVPLIGEYLVFMIFVLISIMVTFA				
	NEGKICLCTSVLSUTVPLLVIEIIIPSSKRVPLIGEYLVFMIFVLISIMVTFA				
	INTHRSSSTHNAAPLVKRIPLHTLPKLCMRSHVDRYFTQKEETESGSGPKSSRT				
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3'UTR	1562..1828				
BASE COUNT	496 a 372 c 419 g 541 t				
ORIGIN					
Query Match	100.0%;	Score 1828;	DB 6;	Length 1828;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1828;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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QY	61	CGACTCACACTAGTCTGATTTCCCAAGAGTTCGGTTCCCGCGCGGGTCCGAG	120		
Db	61	CGACTCACACTAGTCTGATTTCCCAAGAGTTCGGTTCCCGCGCGGGTCCGAG	120		
QY	121	GCGGCTGCCCGCGGTCCCGCGCGGGCGCGGCGCATGGCGCGCGGGGTCA	180		
Db	121	GCGGCTGCCCGCGGTCCCGCGCGGGCGCGGCGCATGGCGCGCGGGGTCA	180		
QY	181	CGCGCTCCGCGTCTGCTCTTGTGTCAGTCTGTCGGCGGCGCTAGCGGCGC	240		
Db	181	CGCGCTCCGCGTCTGCTCTTGTGTCAGTCTGTCGGCGGCGCTAGCGGCGC	240		
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Db	241	GGCGGGGGCGCGCAGAGAGATTACTGAACCTTCTTCTATTGCAAAACATGAAG	300		
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QY	361	TGACAAATATAAATAAATTTGGACTTGCAATATCTCAATTTGGTGATTTGGAT	420		

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959	CTTCTATCTTCTTCAAAATGAAGGTGAAAGATTTTCTCTGCACTTCACTTCTGTGTC	1018
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1447	TCTGTGGAATTTCTTTTTCGTTTCAATTCGATTCGATCTCTTGGCTTTTGTTCCTGTTAT	1506
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RESULT 8		
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DEFINITION	H.sapiens nicotinic receptor alpha 5 subunit mRNA, complete cds.	PRI 31-DEC-1994
ACCESSION	M83712	
VERSION	M83712.1	GI:177925
KEYWORDS	nicotinic receptor alpha 5 subunit.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 1679)	
	Chini, B., Clementi, P., Hukovic, N. and Sher, E.	
	Neuronal-type alpha-bungarotoxin receptors and the alpha	
	5-nicotinic receptor subunit gene are expressed in neuronal and	
	nonneuronal human cell lines	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (5). 1572-1576 (1992)	


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QY 1235 CCMAACTGCTTTGCGATGAGAGTCTGTAGACAGGTACTTCTACTCAGAAAGAGGAAACT 1294
Db 1081 CCMAACTGCTTTGCGATGAGAGTCTGTAGACAGGTACTTCTACTCAGAAAGAGGAAACT 1140
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DEFINITION Bos taurus neuronal nicotinic acetylcholine receptor alpha5 subunit
mRNA, complete cds.
ACCESSION AF487464
VERSION AF487464.1
KEYWORDS GI:19423863
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bos taurus
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1645)
Campos-Caro, A., Smillie, F. I., Dominguez del Toro, E., Rovira, J. C.,
Vicente-Agullo, F., Chapuli, J., Juiz, J. M., Sala, S., Sala, F.,
Ballesta, J. J. and Criado, M.
Neuronal nicotinic acetylcholine receptors on bovine chromaffin
cells: cloning, expression, and genomic organization of receptor
subunits
J. Neurochem. 68 (2), 488-497 (1997)
97156643
MEDLINE 9003033
PUBMED
REFERENCE 2 (bases 1 to 1645)
Campos-Caro, A. and Criado, M.
Direct Submission
Submitted (25-FEB-2002) Biochimica y Biologia Molecular, Instituto
de Neurociencias, CSIC-UMH, Ctra. Valencia-Alicante Km 87, San
Juan, Alicante 03550, Spain
JOURNAL Location/Qualifiers
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Best Local Similarity 85.3%; Pred. No. 2.1e-249;
Matches 1385; Conservative 0; Mismatches 213; Indels 25; Gaps 2;
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RESULT 12

AF204689

LOCUS

AF204689 1445 bp mRNA linear ROD 22-DEC-1999

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DEFINITION Mus musculus nicotinic acetylcholine receptor alpha 5 subunit
ACCESSION AF204689
VERSION AF204689.1 GI:6625910
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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AUTHORS Stitzel,J.A. and Blanchette,J.M.
TITLE Cloning of mouse nicotinic receptor alpha 5 subunit cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1445)
AUTHORS Stitzel,J.A. and Blanchette,J.M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-1999) Pharmacology, University of Michigan, 1500
E. Medical Center Drive CCGC 2150, Ann Arbor, MI 48109-0930, USA
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RESULT 13
CHKAS5SUBULOCUS
DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

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Couturier, S., Erkman, L., Valera, S., Rungger, D., Bertrand, S.,
Boulter, J., Ballivet, M., and Bertrand, D.Alpha 5, alpha 3, and non-alpha 3. Three clustered avian genes
encoding neuronal nicotinic acetylcholine receptor-related subunits
J. Biol. Chem. 265 (29), 17560-17567 (1990)91009210
1698777
Original source text: Chicken cDNA to mRNA and DNA.
Draft entry and computer-readable sequence for [J. Biol. Chem.
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AUTHORS Duga, S., Solda, G., Asselta, R., Bonati, M.T., Dalpra, L., Malcovati, M. and Tenchini, M.L.			
TITLE Characterization of the genomic structure of human nicotinic acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of two novel introns in the 3' untranslated region of CHRNA3 and of a tail-to-tail overlap between CHRNA3 and CHRNA5			
JOURNAL Unpublished			
REFERENCE 2 (bases 1 to 1526)			
AUTHORS Duga, S.			
TITLE Direct Submission			
JOURNAL Submitted (16-MAR-2001) Duga S., Dept. Biology and Genetics for Medical Sciences, University of Milan, via Viotti 3/5, 20133, ITALY			
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DEFINITION Homo sapiens, clone IMAGE:6189913, mRNA.
ACCESSION BC050469

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BC050469.1 GI:29791534
Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2194)
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 98 Row: 1 Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
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/lab_host="DH10B"
/notes="vector: pCMV-SPORT6"
BASE COUNT 744 a 460 c 390 g 600 t
ORIGIN
Query Match 45.9%; Score 838.2; DB 9; Length 2194;
Best Local Similarity 98.5%; Pred. No. 4e-169;
Matches 846; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Db 1489 ATATGTGTGTTATTTAGTGCAGATGGAGGTTTGAAGGAGCAGTACGAAACAGTCAATC 1430
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Dossier: 09743674

Legal Date: 01-28-2004

No.	Doccode	Number of pages
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Total number of pages: 106

Remarks:

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